

PCT/AU2004/001051



REC'D 02 SEP 2004

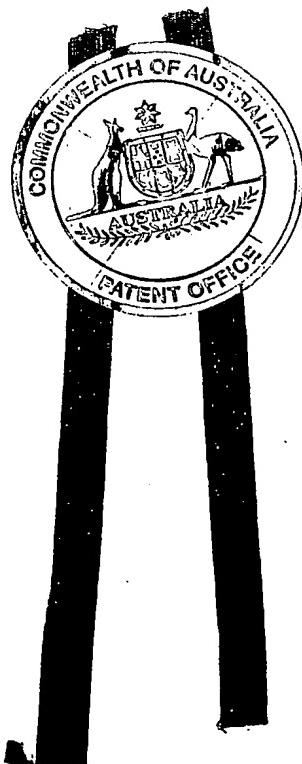
WIPO PCT

Patent Office
Canberra

I, JULIE BILLINGSLEY, TEAM LEADER EXAMINATION SUPPORT AND SALES hereby certify that annexed is a true copy of the Provisional specification in connection with Application No. 2003904154 for a patent by BIONOMICS LIMITED as filed on 07 August 2003.

WITNESS my hand this
Seventeenth day of August 2004

JULIE BILLINGSLEY
TEAM LEADER EXAMINATION
SUPPORT AND SALES



**PRIORITY
DOCUMENT**

SUBMITTED OR TRANSMITTED IN
COMPLIANCE WITH RULE 17.1(a) OR (b)

AUSTRALIA

Patents Act 1990

PROVISIONAL SPECIFICATION

Applicant:

BIONOMICS LIMITED
A.C.N. 075 582 740

Invention Title:

MUTATIONS IN ION CHANNELS

The invention is described in the following statement:

MUTATIONS IN ION CHANNELS

Technical Field

The present invention is concerned with mutations in proteins having biological functions as ion channels and, more particularly, with such mutations where they are associated with diseases such as epilepsy and disorders associated with ion channel dysfunction including, but not restricted to, hyper- or hypo-kalemic periodic paralysis, myotonias, malignant hyperthermia, myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's disease, Parkinson's disease, schizophrenia, hyperekplexia, anxiety, depression, phobic obsessive symptoms, neuropathic pain, inflammatory pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease, Dent's disease, hyperinsulinemic hypoglycemia of infancy, cystic fibrosis, congenital stationary night blindness and total colour-blindness.

20 Background Art

Epilepsies constitute a diverse collection of brain disorders that affect about 3% of the population at some time in their lives (Annegers, 1996). An epileptic seizure can be defined as an episodic change in behaviour caused by the disordered firing of populations of neurons in the central nervous system. This results in varying degrees of involuntary muscle contraction and often a loss of consciousness. Epilepsy syndromes have been classified into more than 40 distinct types based upon characteristic symptoms, types of seizure, cause, age of onset and EEG patterns (Commission on Classification and Terminology of the International League Against Epilepsy, 1989). However the single feature that is common to all syndromes is the persistent increase in neuronal excitability that is both occasionally and unpredictably expressed as a seizure.

A genetic contribution to the aetiology of epilepsy has been estimated to be present in approximately 40% of

affected individuals (Gardiner, 2000). As epileptic seizures may be the end-point of a number of molecular aberrations that ultimately disturb neuronal synchrony, the genetic basis for epilepsy is likely to be 5 heterogeneous. There are over 200 Mendelian diseases which include epilepsy as part of the phenotype. In these diseases, seizures are symptomatic of underlying neurological involvement such as disturbances in brain structure or function. In contrast, there are also a 10 number of "pure" epilepsy syndromes in which epilepsy is the sole manifestation in the affected individuals. These are termed idiopathic and account for over 60% of all epilepsy cases.

Idiopathic epilepsies have been further divided into 15 partial and generalized sub-types. Partial (focal or local) epileptic fits arise from localized cortical discharges, so that only certain groups of muscles are involved and consciousness may be retained. However, in generalized epilepsy, EEG discharge shows no focus such 20 that all subcortical regions of the brain are involved. Although the observation that generalized epilepsies are frequently inherited is understandable, the mechanism by which genetic defects, presumably expressed constitutively in the brain, give rise to partial seizures is less clear.

The molecular genetic era has resulted in spectacular 25 advances in classification, diagnosis and biological understanding of numerous inherited neurological disorders including muscular dystrophies, familial neuropathies and spinocerebellar degenerations. These disorders are all 30 uncommon or rare and have simple Mendelian inheritance. In contrast, common neurological diseases like epilepsy, have complex inheritance where they are determined by multiple genes sometimes interacting with environmental influences. Molecular genetic advances in disorders with 35 complex inheritance have been far more modest to date (Todd, 1999).

Most of the molecular genetic advances have occurred by a sequential three stage process. First a clinically homogeneous disorder is identified and its mode of inheritance determined. Second, linkage analysis is performed on carefully characterized clinical populations with the disorder. Linkage analysis is a process where the chromosomal localization of a particular disorder is narrowed down to approximately 0.5% of the total genome. Knowledge of linkage imparts no intrinsic biological insights other than the important clue as to where to look in the genome for the abnormal gene. Third, strategies such as positional cloning or the positional candidate approach are used to identify the aberrant gene and its specific mutations within the linked region (Collins, 1995).

Linkage studies in disorders with complex inheritance have been bedevilled by negative results and by failure to replicate positive findings. A sense of frustration permeates current literature in the genetics of complex disorders. Carefully performed, large scale studies involving hundreds of sibpairs in disorders including multiple sclerosis and diabetes have been essentially negative (Bell and Lathrop, 1996; Lernmark and Ott, 1998). An emerging view is that such disorders are due to the summation of many genes of small effect and that identification of these genes may only be possible with very large-scale association studies. Such studies on a genome-wide basis are currently impossible due to incomplete marker sets and computational limitations.

The idiopathic generalized epilepsies (IGE) are the most common group of inherited human epilepsy and do not have simple inheritance. Like other complex disorders, linkage studies in IGE have generated controversial and conflicting claims. Previous authors have suggested the possibility of multifactorial, polygenic, oligogenic or two locus models for the disease (Andermann, 1982; Doose

and Baier, 1989; Greenberg et al., 1988a; 1992; Janz et al., 1992).

Two broad groups of IGE are now known - the classical idiopathic generalized epilepsies (Commission on
5 Classification and Terminology of the International League Against Epilepsy, 1989) and the newly recognized genetic syndrome of generalized epilepsy with febrile seizures plus (GEFS⁺) (Scheffer and Berkovic, 1997; Singh et al., 1999).

10 The classical IGEs are divided into a number of clinically recognizable but overlapping sub-syndromes including childhood absence epilepsy, juvenile absence epilepsy, juvenile myoclonic epilepsy etc (Commission on Classification and Terminology of the International League
15 Against Epilepsy, 1989; Roger et al., 1992). The sub-syndromes are identified by age of onset and the pattern of seizure types (absence, myoclonus and tonic-clonic). Some patients, particularly those with tonic-clonic seizures alone do not fit a specifically recognized sub-syndrome. Arguments for regarding these as separate syndromes, yet recognizing that they are part of a neurobiological continuum, have been presented previously
20 (Berkovic et al. 1987; 1994; Reutens and Berkovic, 1995).

25 GEFS⁺ was originally recognized through large multi-generation families and comprises a variety of sub-syndromes. Febrile seizures plus (FS⁺) is a sub-syndrome where children have febrile seizures occurring outside the age range of 3 months to 6 years, or have associated febrile tonic-clonic seizures. Many family members have a
30 phenotype indistinguishable from the classical febrile convulsion syndrome and some have FS⁺ with additional absence, myoclonic, atonic, or complex partial seizures. The severe end of the GEFS⁺ spectrum includes myoclonic-astatic epilepsy.

35 The cumulative incidence for epilepsy by age 30 years (proportion suffering from epilepsy at some time) is 1.5% (Hauser et al., 1993). Accurate estimates for the

- cumulative incidence of the IGEs are unavailable. In epidemiological studies where attempts are made to subclassify epilepsies, rather few cases of IGE are diagnosed, and many cases are unclassified. This is probably because cases are rarely directly examined by epileptologists. In clinic- or office-based series seen by experts, most cases are classifiable and IGEs account for about 25% of cases. This suggests that about 0.3% of the population suffer from IGE at some time.
- In outbred populations many patients with classical IGE appear to be sporadic as siblings and parents are usually unaffected. Systematic EEG studies on clinically unaffected family members show an increase in age-dependent occurrence of generalized epileptiform discharges compared to controls. In addition, to the approximate 0.3% of the population with clinical IGE, systematic EEG studies suggest that about 1% of healthy children have generalized epileptiform discharges while awake (Cavazzuti et al., 1980; Okubo et al., 1994).
- Approximately 5-10% of first degree relatives of classical IGE probands have seizures with affected relatives usually having IGE phenotypes or febrile seizures. While nuclear families with 2-4 affected individuals are well recognized and 3 generation families or grandparent-grandchild pairs are occasionally observed (Italian League Against Epilepsy Genetic Collaborative Group, 1993), families with multiple affected individuals extending over 4 or more generations are exceptionally rare.
- For GEFS⁺, however, a number of large multi-generation families showing autosomal dominant inheritance with incomplete penetrance are known. Similar to classical IGE, analysis of sporadic cases and small families with GEFS⁺ phenotypes does not suggest simple Mendelian inheritance. Indeed, bilineal inheritance, where there is a history of epilepsy on maternal and paternal sides, is observed in both GEFS⁺ and classical IGE families (Singh et al., 1999;

Italian League Against Epilepsy Genetic Collaborative Group, 1993).

Within single families with classical IGE or GEFS⁺, affected individuals often have different sub-syndromes.

- 5 The closer an affected relative is to the proband, the more similar are their sub-syndromes, and siblings often have similar sub-syndromes (Italian League Against Epilepsy Genetic Collaborative Group, 1993). Less commonly, families are observed where most, or all, known
10 affected individuals have one classical IGE sub-syndrome such as childhood absence epilepsy or juvenile myoclonic epilepsy (Italian League Against Epilepsy Genetic Collaborative Group, 1993).

Importantly, sub-syndromes are identical in affected
15 monozygous twins with IGE. In contrast, affected dizygous twins, may have the same or different sub-syndromes. Classical IGE and GEFS⁺ sub-syndromes tend to segregate separately (Singh et al., 1999).

In some inbred communities, pedigree analysis
20 strongly suggests recessive inheritance for juvenile myoclonic epilepsy and other forms of IGE (Panayiotopoulos and Obeid, 1989; Berkovic et al., 2000). In such families, sub-syndromes are much more similar in affected siblings than in affected sib-pairs from outbred families.
25 Recently, a family with an infantile form of IGE with autosomal recessive inheritance, confirmed by linkage analysis, was described in Italy (Zara et al., 2000).

Most work on the molecular genetics of classical IGEs has been done on the sub-syndrome of juvenile myoclonic epilepsy where a locus in proximity or within the HLA region on chromosome 6p was first reported in 1988
30 (Greenberg et al., 1988b). This finding was supported by two collaborating laboratories, in separate patient samples, and subsequently three groups provided further evidence for a 6p locus for juvenile myoclonic epilepsy in some, but not all, of their families. However, genetic defects have not been found and the exact locus of the
35

gene or genes, in relationship to the HLA region, remains controversial. Strong evidence for linkage to chromosome 6 also comes from a study of a single large family with juvenile myoclonic epilepsy, but in this pedigree the 5 locus is well outside the HLA region. A locus on chromosome 15q has also been suggested for juvenile myoclonic epilepsy, but was not confirmed by two other studies.

In general, the results of studies of the putative 10 chromosomal 6p locus in the HLA region in patients with absence epilepsies or other forms of idiopathic generalized epilepsies have been negative. The major exception is that study of probands with tonic-clonic seizures on awakening, a sub-syndrome closely related to 15 juvenile myoclonic epilepsy, suggests linkage to 6p.

Linkage for classical remitting childhood absence epilepsy remains elusive, but in a family with persisting absence evolving into a juvenile myoclonic epilepsy phenotype, linkage to chromosome 1p has been claimed. An 20 Indian pedigree with persisting absence and tonic-clonic seizures may link to 8q24. Linkage to this region was also suggested by a non-parametric analysis in IGE, irrespective of subsyndrome, but was not confirmed in another study. Other loci for IGEs that have been reported 25 in single studies include 3p14, 8p, 18 and possibly 5p. The unusual example of recessively inherited infantile onset IGE described in Italy maps to 16p in a single family.

Thus, like most disorders with complex inheritance, 30 the literature on genetics of classical IGEs is confusing and contradictory. Some, and perhaps much, of this confusion is due to heterogeneity, with the likelihood of a number of loci for IGEs. The studies reviewed above were principally performed on multiple small families, so 35 heterogeneity within and between samples is probable. Whether all, some, or none of the linkages reported above will be found to harbour relevant genes for IGE remains to

be determined. Most of the studies reviewed above used analysis methods assuming Mendelian inheritance, an assumption that is not correct for outbred communities. Some studies used multiple models (autosomal recessive, 5 autosomal dominant). Although parametric linkage analysis may be reliable in some circumstance of analyzing complex disease, it can lead to spurious findings as highlighted by the literature on linkage in major psychoses (Risch and Botstein, 1996).

10 In so far as GEFS⁺ is concerned, linkage analysis on rare multi-generation large families with clinical evidence of a major autosomal dominant gene have demonstrated loci on chromosomes 19q and 2q. Both the 19q and 2q GEFS⁺ loci have been confirmed in independently 15 ascertained large families, and genetic defects have been identified. Families linked to 19q are known and a mutation in the gene for the $\beta 1$ subunit of the neuronal sodium channel (SCN1B) has been identified (Wallace et al., 1998). This mutation results in the loss of a 20 critical disulphide bridge of this regulatory subunit and causes a loss of function in vitro. Families linked to 2q are also known and mutations in the pore-forming α subunit of the neuronal sodium channel (SCN1A) have been identified (PCT/AU01/01648; Wallace et al., 2001b; Escayg 25 et al., 2000). Studies on the more common small families with GEFS⁺ have not revealed these or other mutations to date.

In addition to the SCN1B and SCN1A mutations in GEFS⁺, four other gene defects have been discovered for human 30 idiopathic epilepsies through the study of large families. Mutations in the alpha-4 subunit of the neuronal nicotinic acetylcholine receptor (CHRNA4) occur in the focal epilepsy syndrome of autosomal dominant nocturnal frontal lobe epilepsy (Australian patent AU-B-56247/96; Steinlein 35 et al., 1995). Mutations in the gamma-2 subunit of the GABA_A receptor (GABRG2) have been identified in childhood absence epilepsy, febrile seizures (including febrile

seizures plus) and myoclonic epilepsy (PCT/AU01/00729; Wallace et al., 2001a). Finally, mutations in two potassium channel genes (KCNQ2 and KCNQ3) were identified in benign familial neonatal convulsions (Singh et al., 5 1998; Biervert et al., 1998; Charlier et al., 1998). Although initially regarded as a special form of IGE, this unusual syndrome is probably a form of inherited focal epilepsy.

Further to these studies, mutations in other genes 10 have been identified to be causative of epilepsy. These include mutations in the beta-2 subunit (CHRNB2) of the neuronal nicotinic acetylcholine receptor (PCT/AU01/00541; Phillips et al., 2001) and the delta subunit (GABRD) of the GABA_A receptor (PCT/AU01/00729).

15 A number of mouse models approximating human IGE are known. These mice mutants have ataxia in addition to generalized spike-and-wave discharges with absences or tonic-clonic seizures. Recessive mutations in calcium channel subunit genes have been found in lethargic 20 (CACNB4), tottering/leaner (CACNA1A), and stargazer (CACNG2) mutants. The slow-wave epilepsy mouse mutant has a mutation in the sodium/hydrogen exchanger gene, which may have important downstream effects on pH-sensitive ion channels.

25 The human and mouse literature is now suggesting that the idiopathic epilepsies comprise a family of channelopathies with mutations in ion channel subunits of voltage-gated (eg SCN1A, SCN1B, KCNQ2, KCNQ3) or ligand-gated (eg CHRNA4, CHRNB2, GABRG2, GABRD) types. These 30 channels are typically comprised of a number of subunits, specified by genes on different chromosomes. The stoichiometry and conformation of ion channel subunits are not yet well understood, but many have multiple subunits in a variety of combinations.

35 The involvement of ion channels in other neuro/physiological disorders has also been observed (reviewed in Dworakowska and Dolowy, 2000). Mutations in

voltage-gated sodium, potassium, calcium and chloride channels as well as ligand-gated channels such as the acetylcholine and GABA receptors may lead to physiological disorders such as hyper- and hypo-kalemic periodic 5 paralysis, myotonias, malignant hyperthermia, myasthenia and cardiac arrhythmias. Neurological disorders other than epilepsy that are associated with ion channel mutations include episodic ataxia, migraine, Alzheimer's disease, Parkinson's disease, schizophrenia, hyperekplexia, 10 anxiety, depression, phobic obsessive symptoms, as well as neuropathic pain, inflammatory pain and chronic/acute pain. Some kidney disorders such as Bartter's syndrome, polycystic kidney disease and Dent's disease, secretion 15 disorders such as hyperinsulinemic hypoglycemia of infancy and cystic fibrosis, and vision disorders such as congenital stationary night blindness and total colour-blindness may also be linked to mutations in ion channels.

Disclosure of the Invention

20 In a new genetic model for the idiopathic generalised epilepsies (IGEs) described in PCT/AU01/00872 (the disclosure of which is incorporated herein by reference) it has been postulated that most classical IGE and GEFs⁺ cases are due to the combination of two mutations in 25 multi-subunit ion channels. These are typically point mutations resulting in a subtle change of function. The critical postulate is that two mutations, usually, but not exclusively, in different subunit alleles ("digenic model"), are required for clinical expression of IGE. It 30 was further proposed that

- a) A number of different mutated subunit pairs can be responsible for IGE. Combinations of two mutated subunits lead to an IGE genotype with ~30% penetrance.
- 35 b) The total allele frequency of mutated subunits is ~8%. It was calculated that approximately 15% of the population has one or more mutated

- subunit genes and 1% have two or more mutated subunits.
- c) Sub-syndromes are principally determined by the specific combination of mutated subunit pairs, although one or more other genes, including ion channel subunits, of smaller effect may modify the phenotype.
- d) Mutated subunit combinations that cause classical IGEs are largely separate from those that cause GEFS⁺, although some subunits may be involved in both syndromes.
- e) Individuals with single 'change of function' mutations would not have IGE, but such mutations may contribute to simple febrile seizures, which are observed with increased frequency in relatives of IGE probands.

The model also proposes that subunit mutations with more severe functional consequences (eg breaking a disulphide bridge in SCN1B or amino acid substitution in the pore forming regions of SCN1A for GEFS⁺) cause autosomal dominant generalized epilepsies with a penetrance of 60-90%. The precise sub-syndromes in GEFS⁺ are determined by minor allelic variation or mutations in other ion channel subunits. Such "severe" mutations are rare (allele frequency <0.01%) and are infrequent causes of GEFS⁺. They very rarely, or perhaps never, cause classical IGE.

The identification of molecular changes in ion channel subunits is therefore a significant step towards the elucidation of genetic variants that alone or in combination (based on the digenic model) give rise to an epilepsy phenotype, and to other neuro/physiological disorders associated with ion channel dysfunction.

The present inventors have identified a number of novel mutations or variants in genes encoding subunits of ion channels in individuals with epilepsy. It will be appreciated that for each molecular defect one can provide

an isolated nucleic acid molecule coding for a protein having a biological function as part of an ion channel in a mammal, wherein a mutation event selected from the group consisting of point mutations, deletions, insertions and rearrangements has occurred so as to affect the functioning of the ion channel. In some instances this single mutation alone will produce a phenotype of epilepsy or other neuro/physiological disorders associated with ion channel dysfunction.

In the case where a single mutation alone does not produce, say, an epilepsy phenotype, there would be provided one or more additional isolated nucleic acid molecules coding for proteins having a biological function as part of an ion channel in a mammal, wherein a mutation event selected from the group consisting of point mutations, deletions, insertions and rearrangements has occurred so as to affect the functioning of the ion channel. The cumulative effect of the mutations in each isolated nucleic acid molecule *in vivo* is to produce a epilepsy or another neuro/physiological disorders in said mammal. The mutations may be in nucleic acid molecules coding for protein subunits belonging to the same ion channel or may be in nucleic acid molecules coding for protein subunits that belong to different ion channels.

Typically such mutations are point mutations and the ion channels are voltage-gated channels such as a sodium, potassium, calcium or chloride channels or are ligand-gated channels such as members of the nAChR/GABA super family of receptors, or a functional fragment or homologue thereof.

Mutations may include those in non-coding regions of the ion channel subunits (eg mutations in the promoter region which affect the level of expression of the subunit gene, mutations in intronic sequences which affect the correct splicing of the subunit during mRNA processing, or mutations in the 5' or 3' untranslated regions that can affect translation or stability of the mRNA). Mutations

may also and more preferably will be in coding regions of the ion channel subunits (eg nucleotide mutations may give rise to an amino acid change in the encoded protein or nucleotide mutations that do not give rise to an amino acid change but may affect the stability of the mRNA).

5 Mutation combinations may be selected from, but are not restricted to, those identified in Table 1.

Accordingly in one aspect of the present invention there is provided a method of identifying a subject 10 predisposed to a disorder associated with ion channel dysfunction, comprising ascertaining whether at least one of the genes encoding ion channel subunits in said subject has undergone a mutation event as set forth in one of SEQ ID Numbers: 1-62.

15 In another aspect of the present invention there is provided an isolated nucleic acid molecule encoding a mutant or variant ion channel subunit wherein a mutation event has occurred as set forth in one of SEQ ID Numbers: 1-62.

20 The mutation event disrupts the functioning of an ion channel so as to produce a phenotype of epilepsy; and/or one or more other disorders associated with ion channel dysfunction, including but not restricted to, hyper- or hypo-kalemic periodic paralysis, myotonias, malignant 25 hyperthermia, myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's disease, Parkinson's disease, schizophrenia, hyperekplexia, anxiety, depression, phobic obsessive symptoms, neuropathic pain, inflammatory pain, chronic/acute pain, Bartter's syndrome, 30 polycystic kidney disease, Dent's disease, hyperinsulinemic hypoglycemia of infancy, cystic fibrosis, congenital stationary night blindness and total colour-blindness, either alone or in combination with one or more additional mutations or variations in the ion channel 35 subunit genes.

In another aspect of the present invention there is provided an isolated nucleic acid molecule encoding a

mutant KCNQ2 subunit, wherein the mutation event has occurred in the C-terminal domain of the KCNQ2 subunit and leads to a disturbance in the calmodulin binding affinity of the subunit, so as to produce an epilepsy phenotype.

5 In one form of the invention, the mutations are in exon 8 or exon 15 of the KCNQ2 subunit and result in the replacement of an arginine residue with a glycine residue at amino acid position 353, or the replacement of a leucine residue with an arginine at amino acid position
10 619. The R353G mutation occurs as a result of a C to G nucleotide substitution at position 1057 of the KCNQ2 coding sequence as shown in SEQ ID NO: 34. The L619R mutation occurs as a result of a T to G nucleotide substitution at position 1856 of the KCNQ2 coding sequence
15 as shown in SEQ ID NO: 37.

In a further form of the invention, the mutations are in exon 11 or exon 14 of the KCNQ2 subunit and result in the replacement of an arginine residue with a stop codon at amino acid position 430, or the replacement of an arginine residue with a serine at amino acid position 570. The R430X mutation occurs as a result of a C to T nucleotide substitution at position 1288 of the KCNQ2 coding sequence as shown in SEQ ID NO: 35. The R570S mutation occurs as a result of an A to T nucleotide substitution at position 1710 of the KCNQ2 coding sequence
25 as shown in SEQ ID NO: 36.

Typically these mutations create a phenotype of benign familial neonatal seizures (BFNS).

In a further aspect of the present invention there is
30 provided a combination of two or more isolated nucleic acid molecules each having a novel mutation event as laid out in Table 1. The cumulative effect of the mutations in each isolated nucleic acid molecule *in vivo* is to produce an epilepsy or another disorder associated with ion channel dysfunction as described above in said mammal.
35

In a particularly preferred embodiment of the present invention, the isolated nucleic acid molecules have a

nucleotide sequence as shown in any one of SEQ ID Numbers: 1-62. The sequences correspond to the novel DNA mutations or variants laid out in Table 1.

5 In another aspect of the present invention there is provided an isolated nucleic acid molecule comprising any one of the nucleotide sequences set forth in SEQ ID Numbers: 1-62.

10 In another aspect of the present invention there is provided an isolated nucleic acid molecule consisting of any one of the nucleotide sequences set forth in SEQ ID Numbers: 1-62.

15 The nucleotide sequences of the present invention can be engineered using methods accepted in the art for a variety of purposes. These include, but are not limited to, modification of the cloning, processing, and/or expression of the gene product. PCR reassembly of gene fragments and the use of synthetic oligonucleotides allow the engineering of the nucleotide sequences of the present invention. For example, oligonucleotide-mediated site-directed mutagenesis can introduce further mutations that create new restriction sites, alter expression patterns 20 and produce splice variants etc.

25 As a result of the degeneracy of the genetic code, a number of polynucleotide sequences, some that may have minimal similarity to the polynucleotide sequences of any known and naturally occurring gene, may be produced. Thus, the invention includes each and every possible variation 30 of a polynucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the polynucleotide sequences of the present invention, and all such variations are to be considered as being specifically disclosed.

35 The nucleic acid molecules of this invention are typically DNA molecules, and include cDNA, genomic DNA, synthetic forms, and mixed polymers, both sense and

antisense strands, and may be chemically or biochemically modified, or may contain non-natural or derivatised nucleotide bases as will be appreciated by those skilled in the art. Such modifications include labels,
5 methylation, intercalators, alkylators and modified linkages. In some instances it may be advantageous to produce nucleotide sequences possessing a substantially different codon usage than that of the polynucleotide sequences of the present invention. For example, codons
10 may be selected to increase the rate of expression of the peptide in a particular prokaryotic or eukaryotic host corresponding with the frequency that particular codons are utilized by the host. Other reasons to alter the nucleotide sequence without altering the encoded amino
15 acid sequences include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring mutated sequence.

The invention also encompasses production of nucleic acid sequences of the present invention entirely by synthetic chemistry. Synthetic sequences may be inserted into expression vectors and cell systems that contain the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. These elements may include regulatory sequences, promoters, 5' and 3' untranslated regions and specific initiation signals (such as an ATG initiation codon and Kozak consensus sequence) which allow more efficient translation of sequences encoding the polypeptides of the present invention. In cases where the complete coding sequence, including the initiation codon and upstream regulatory sequences, are inserted into the appropriate expression vector, additional control signals may not be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals as described above should be provided by the vector. Such signals may be of various origins, both

natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate for the particular host cell system used (Scharf et al., 1994).

The invention also includes nucleic acid molecules
5 that are the complements of the sequences described herein.

The present invention allows for the preparation of purified polypeptide or protein from the polynucleotides of the present invention, or variants thereof. In order to
10 do this, host cells may be transformed with a novel nucleic acid molecule as described above, or with nucleic acid molecules encoding two or more mutant ion channel subunits. If the mutant subunits form a part of the same ion channel a receptor protein containing two or more
15 mutant subunits may be isolated. If the mutant subunits are subunits of different ion channels the host cells will express two or more mutant receptor proteins. Typically said host cells are transfected with an expression vector comprising a DNA molecule according to the invention or,
20 in particular, DNA molecules encoding two or more mutant ion channel subunits. A variety of expression vector/host systems may be utilized to contain and express sequences encoding polypeptides of the invention. These include, but are not limited to, microorganisms such as bacteria
25 transformed with plasmid or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); or mouse or other animal or human tissue cell systems. Mammalian cells can also be used to express
30 a protein using a vaccinia virus expression system. The invention is not limited by the host cell or vector employed.

The polynucleotide sequences, or variants thereof, of the present invention can be stably expressed in cell
35 lines to allow long term production of recombinant proteins in mammalian systems. Sequences encoding the polypeptides of the present invention can be transformed

into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. The selectable marker confers resistance to a selective agent, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be propagated using tissue culture techniques appropriate to the cell type.

The protein produced by a transformed cell may be secreted or retained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode a protein may be designed to contain signal sequences which direct secretion of the protein through a prokaryotic or eukaryotic cell membrane.

In addition, a host cell strain may be chosen for its ability to modulate expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, glycosylation, phosphorylation, and acylation. Post-translational cleavage of a "prepro" form of the protein may also be used to specify protein targeting, folding, and/or activity. Different host cells having specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO or HeLa cells), are available from the American Type Culture Collection (ATCC) and may be chosen to ensure the correct modification and processing of the foreign protein.

When large quantities of the protein product of the gene are needed, such as for antibody production, vectors which direct high levels of expression of this protein may be used, such as those containing the T5 or T7 inducible bacteriophage promoter. The present invention also includes the use of the expression systems described above in generating and isolating fusion proteins which contain

important functional domains of the protein. These fusion proteins are used for binding, structural and functional studies as well as for the generation of appropriate antibodies.

5 In order to express and purify the protein as a fusion protein, the appropriate cDNA sequence is inserted into a vector which contains a nucleotide sequence encoding another peptide (for example, glutathione succinyl transferase). The fusion protein is expressed and
10 recovered from prokaryotic or eukaryotic cells. The fusion protein can then be purified by affinity chromatography based upon the fusion vector sequence. The desired protein is then obtained by enzymatic cleavage of the fusion protein.

15 Fragments of the polypeptides of the present invention may also be produced by direct peptide synthesis using solid-phase techniques. Automated synthesis may be achieved by using the ABI 431A Peptide Synthesizer (Perkin-Elmer). Various fragments of this protein may be
20 synthesized separately and then combined to produce the full-length molecule.

The present invention is also concerned with polypeptides having a biological function as an ion channel in a mammal, wherein a mutation event selected
25 from the group consisting of substitutions, deletions, truncations, insertions and rearrangements has occurred so as to affect the functioning of the ion channel. In some instances this single mutation alone will produce an epilepsy phenotype or other neuro/physiological disorders
30 associated with ion channel dysfunction.

In the case where a single mutation alone does not produce, say, an epilepsy phenotype, there would be provided one or more additional isolated mammalian polypeptides having biological functions as part of an ion
35 channel in a mammal, wherein a mutation event selected from the group consisting of substitutions, deletions, truncations, insertions and rearrangements has occurred so

as to affect the functioning of the ion channel. The cumulative effect of the mutations in each isolated mammalian polypeptide *in vivo* being to produce epilepsy or another neuro/physiological disorders in said mammal. The 5 mutations may be in polypeptide subunits belonging to the same ion channel as described above, but may also be in polypeptide subunits that belong to different ion channels.

Typically the mutation is an amino acid substitution 10 and the ion channel is a voltage-gated channel such as a sodium, potassium, calcium or chloride channel or a ligand-gated channel such as a member of the nAChR/GABA super family of receptors, or a functional fragment or homologue thereof.

15 Mutation combinations may be selected from, but are not restricted to, those represented in Table 1.

Accordingly, in a further aspect of the present invention there is provided an isolated polypeptide, said polypeptide being a mutant or variant ion channel subunit 20 wherein a mutation event has occurred such that the polypeptide has the amino acid sequence set forth in one of SEQ ID Numbers: 63-76. The mutation event disrupts the functioning of an ion channel so as to produce a phenotype of epilepsy, and/or one or more other disorders associated 25 with ion channel dysfunction, including but not restricted to, hyper- or hypo-kalemic periodic paralysis, myotonias, malignant hyperthermia, myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's disease, Parkinson's disease, schizophrenia, hyperekplexia, 30 anxiety, depression, phobic obsessive symptoms, neuropathic pain, inflammatory pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease, Dent's disease, hyperinsulinemic hypoglycemia of infancy, cystic fibrosis, congenital stationary night blindness and total 35 colour-blindness.

In a particularly preferred embodiment of the present invention, the isolated polypeptide has an amino acid

sequence as shown in any one of SEQ ID Numbers: 63-76. The sequences correspond to the novel amino acid changes laid out in Table 1 for those instances where the DNA mutation results in an amino acid change.

5 According to still another aspect of the present invention there is provided an isolated polypeptide, said polypeptide being a mutant KCNQ2 subunit, wherein the mutation event has occurred in the C-terminal domain of the KCNQ2 subunit and leads to a disturbance in the 10 calmodulin binding affinity of the subunit, so as to produce an epilepsy phenotype.

In one form of the invention the mutations are substitutions in which an arginine residue is replaced with a glycine residue, or a leucine residue is replaced 15 with an arginine. Preferably the substitutions are R353G and L619R transitions as illustrated by SEQ ID NOS: 73 and 76 respectively.

In a further form of the invention the mutations result in the replacement of an arginine for a stop codon, 20 or an arginine is replaced with a serine. Preferably the mutations are R430X and R570S transitions as illustrated by SEQ ID NOS: 74 and 75 respectively.

In a still further aspect of the present invention there is provided a combination of two or more isolated 25 polypeptides each having a novel mutation event as laid out in Table 1. The cumulative effect of the mutations in each isolated polypeptide molecule *in vivo* is to produce an epilepsy or another disorder associated with ion channel dysfunction as described above in said mammal.

30 In a particularly preferred embodiment of the present invention, the isolated polypeptides have an amino acid sequence as shown in any one of SEQ ID Numbers: 63-76. The sequences correspond to the novel amino acid changes laid out in Table 1.

35 According to still another aspect of the present invention there is provided an isolated polypeptide

comprising the amino acid sequence set forth in any one of SEQ ID Numbers: 63-76.

According to still another aspect of the present invention there is provided a polypeptide consisting of 5 the amino acid sequence set forth in any one of SEQ ID Numbers: 63-76.

According to still another aspect of the present invention there is provided a method of preparing a polypeptide, comprising the steps of:

- 10 (1) culturing host cells transfected with an expression vector comprising a nucleic acid molecule as described above under conditions effective for polypeptide production; and
- (2) harvesting the mutant ion channel subunit.

15 The mutant ion channel subunit may be allowed to assemble with other subunits constituting the channel that are either wild-type or themselves mutant subunits, whereby the assembled ion channel is harvested.

According to still another aspect of the invention 20 there is provided a polypeptide which is the product of the process described above.

Substantially purified protein or fragments thereof can then be used in further biochemical analyses to establish secondary and tertiary structure. Such 25 methodology is known in the art and includes, but is not restricted to, X-ray crystallography of crystals of the proteins or of the assembled ion channel incorporating the proteins or by nuclear magnetic resonance (NMR). Determination of structure allows for the rational design 30 of pharmaceuticals to interact with the ion channel as a whole or through interaction with a specific subunit protein (see drug screening below), alter the overall ion channel protein charge configuration or charge interaction with other proteins, or to alter its function in the cell.

35 It will be appreciated that the mutant ion channel subunits included as part of the present invention will be useful in further applications which include a variety of

hybridisation and immunological assays to screen for and detect the presence of either a normal or mutated gene or gene product. The invention enables therapeutic methods for the treatment of epilepsy as well as other disorders 5 associated with ion channel dysfunction and also enables methods for the diagnosis of epilepsy as well as other disorders associated with ion channel dysfunction.

Therapeutic Applications

10 According to still another aspect of the invention there is provided a method of treating epilepsy as well as other disorders associated with ion channel dysfunction, including but not restricted to, hyper- or hypo-kalemic periodic paralysis, myotonia, malignant hyperthermia, 15 myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's disease, Parkinson's disease, schizophrenia, hyperekplexia, anxiety, depression, phobic obsessive symptoms, neuropathic pain, inflammatory pain, chronic/acute pain, Bartter's syndrome, polycystic kidney 20 disease, Dent's disease, hyperinsulinemic hypoglycemia of infancy, cystic fibrosis, congenital stationary night blindness or total colour-blindness, comprising administering a selective antagonist, agonist or modulator 25 of an ion channel or ion channel subunit, when the ion channel contains a mutation in a subunit comprising the channel, as described above, to a subject in need of such treatment. Said mutation event may be causative of the disorder when expressed alone or when expressed in combination with one or more additional mutations in 30 subunits of the same or different ion channels, which are typically those identified in Table 1.

In still another aspect of the invention there is provided the use of a selective antagonist, agonist or modulator of an ion channel or ion channel subunit when 35 the ion channel contains a mutation in a subunit comprising the channel, as described above, said mutation being causative of epilepsy as well as other disorders

associated with ion channel dysfunction, including but not restricted to, hyper- or hypo-kalemic periodic paralysis, myotonias, malignant hyperthermia, myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's disease, Parkinson's disease, schizophrenia, hyperekplexia, anxiety, depression, phobic obsessive symptoms, neuropathic pain, inflammatory pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease, Dent's disease, hyperinsulinemic hypoglycemia of infancy, cystic fibrosis, congenital stationary night blindness or total colour-blindness, when expressed alone or when expressed in combination with a second mutation in a subunit of the same or different ion channel, as described above, in the manufacture of a medicament for the treatment of the disorder.

In one aspect, a suitable antagonist, agonist or modulator will restore wild-type function to the ion channel or channels containing the mutations of the present invention, or will negate the effects the mutant channel or channels have on cell function.

Using methods well known in the art, a mutant ion channel may be used to produce antibodies specific for the mutant channel that is causative of the disease or to screen libraries of pharmaceutical agents to identify those that bind the mutant ion channel.

In one aspect, an antibody, which specifically binds to a mutant ion channel or mutant ion channel subunit of the invention, may be used directly as an agonist, antagonist or modulator, or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissues that express the mutant ion channel.

In a still further aspect of the invention there is provided an antibody which is immunologically reactive with a polypeptide as described above, but not with a wild-type ion channel or ion channel subunit thereof.

In particular, there is provided an antibody to an assembled ion channel containing a mutation in a subunit

comprising the receptor, which is causative of epilepsy or another disorder associated with ion channel dysfunction when expressed alone or when expressed in combination with one or more other mutations in subunits of the same or 5 different ion channels. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies as would be understood by the person skilled in the art.

For the production of antibodies, various hosts 10 including rabbits, rats, goats, mice, humans, and others may be immunized by injection with a polypeptide as described above or with any fragment or oligopeptide thereof which has immunogenic properties. Various adjuvants may be used to increase immunological response 15 and include, but are not limited to, Freund's, mineral gels such as aluminium hydroxide, and surface-active substances such as lysolecithin. Adjuvants used in humans include BCG (bacilli Calmette-Guerin) and Corynebacterium parvum.

It is preferred that the oligopeptides, peptides, or 20 fragments used to induce antibodies to the mutant ion channel have an amino acid sequence consisting of at least 5 amino acids, and, more preferably, of at least 10 amino acids. It is also preferable that these oligopeptides, 25 peptides, or fragments are identical to a portion of the amino acid sequence of the natural protein and contain the entire amino acid sequence of a small, naturally occurring molecule. Short stretches of ion channel amino acids may be fused with those of another protein, such as KLH, and 30 antibodies to the chimeric molecule may be produced.

Monoclonal antibodies to a mutant ion channel may be prepared using any technique which provides for the 35 production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique. (For example, see Kohler

et al., 1975; Kozbor et al., 1985; Cote et al., 1983; Cole et al., 1984).

Monoclonal antibodies produced may include, but are not limited to, mouse-derived antibodies, humanised 5 antibodies and fully human antibodies.

Antibodies may also be produced by inducing *in vivo* production in the lymphocyte population or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature. (For 10 example, see Orlandi et al., 1989; Winter and Milstein, 1991).

Antibody fragments which contain specific binding sites for a mutant ion channel may also be generated. For example, such fragments include, F(ab')₂ fragments 15 produced by pepsin digestion of the antibody molecule and Fab fragments generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the 20 desired specificity. (For example, see Huse et al., 1989).

Various immunoassays may be used for screening to identify antibodies having the desired specificity. Numerous protocols for competitive binding or immunoradiometric assays using either polyclonal or 25 monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between an ion channel and its specific antibody. A two-site, monoclonal-based immunoassay utilizing antibodies reactive to two 30 non-interfering ion channel epitopes is preferred, but a competitive binding assay may also be employed.

In a further aspect of the invention there is provided a method of treating epilepsy as well as other disorders associated with ion channel dysfunction, 35 including but not restricted to, hyper- or hypo-kalemic periodic paralysis, myotonias, malignant hyperthermia, myasthenia, cardiac arrhythmias, episodic ataxia,

migraine, Alzheimer's disease, Parkinson's disease, schizophrenia, hyperekplexia, anxiety, depression, phobic obsessive symptoms, neuropathic pain, inflammatory pain, chronic/acute pain, Bartter's syndrome, polycystic kidney
5 disease, Dent's disease, hyperinsulinemic hypoglycemia of infancy, cystic fibrosis, congenital stationary night blindness or total colour-blindness, comprising administering an isolated nucleic acid molecule which is the complement (antisense) of any one of the nucleic acid
10 molecules described above and which encodes an RNA molecule that hybridizes with the mRNA encoding a mutant ion channel subunit of the invention, to a subject in need of such treatment.

In a still further aspect of the invention there is
15 provided the use of an isolated nucleic acid molecule which is the complement (antisense) of a nucleic acid molecule of the invention and which encodes an RNA molecule that hybridizes with the mRNA encoding a mutant ion channel subunit of the invention, in the manufacture
20 of a medicament for the treatment of epilepsy as well as other disorders associated with ion channel dysfunction, including but not restricted to, hyper- or hypo-kalemic periodic paralysis, myotonia, malignant hyperthermia, myasthenia, cardiac arrhythmias, episodic ataxia,
25 migraine, Alzheimer's disease, Parkinson's disease, schizophrenia, hyperekplexia, anxiety, depression, phobic obsessive symptoms, neuropathic pain, inflammatory pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease, Dent's disease, hyperinsulinemic hypoglycemia of infancy, cystic fibrosis, congenital stationary night blindness or total colour-blindness.

Typically, a vector expressing the complement (antisense) of the polynucleotides of the invention may be administered to a subject in need of such treatment. Many
35 methods for introducing vectors into cells or tissues are available and equally suitable for use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be

introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or by polycationic amino polymers may be 5 achieved using methods which are well known in the art. (For example, see Goldman et al., 1997).

Additional antisense or gene-targeted silencing strategies may include, but are not limited to, the use of antisense oligonucleotides, injection of antisense RNA, 10 transfection of antisense RNA expression vectors, and the use of RNA interference (RNAi) or short interfering RNAs (siRNA). Still further, catalytic nucleic acid molecules such as DNAzymes and ribozymes may be used for gene silencing (Breaker and Joyce, 1994; Haseloff and Gerlach, 15 1988). These molecules function by cleaving their target mRNA molecule rather than merely binding to it as in traditional antisense approaches.

In a further aspect, a suitable agonist, antagonist or modulator may include peptides, phosphopeptides or 20 small organic or inorganic compounds that can restore wild-type activity of ion channels containing mutations in the subunits which comprise the channels as described above.

Peptides, phosphopeptides or small organic or 25 inorganic compounds suitable for therapeutic applications may be identified using nucleic acids and peptides of the invention in drug screening applications as described below. Molecules identified from these screens may also be of therapeutic application in affected individuals 30 carrying other ion channel subunit gene mutations if the molecule is able to correct the common underlying functional deficit imposed by these mutations and those of the invention.

There is therefore provided a method of treating 35 epilepsy as well as other disorders associated with ion channel dysfunction comprising administering a compound that is a suitable agonist, antagonist or modulator of an

ion channel and that has been identified using the mutant ion channel subunits of the invention.

In some instances, an appropriate approach for treatment may be combination therapy. This may involve the 5 administering an antibody or complement (antisense) to a mutant ion channel or ion channel subunit of the invention to inhibit its functional effect, combined with administration of wild-type ion channel subunits which may restore levels of wild-type ion channel formation to 10 normal levels. Wild-type ion channel subunits of the invention can be administered using gene therapy approaches as described above for complement administration.

There is therefore provided a method of treating 15 epilepsy as well as other disorders associated with ion channel dysfunction comprising administration of an antibody or complement to a mutant ion channel or ion channel subunit of the invention in combination with administration of wild-type ion channel subunits.

In still another aspect of the invention there is 20 provided the use of an antibody or complement to a mutant ion channel or ion channel subunit of the invention in combination with the use of wild-type ion channel subunits, in the manufacture of a medicament for the 25 treatment of epilepsy as well as other disorders associated with ion channel dysfunction.

In further embodiments, any of the agonists, antagonists, modulators, antibodies, complementary sequences or vectors of the invention may be administered 30 in combination with other appropriate therapeutic agents. Selection of the appropriate agents may be made by those skilled in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or 35 prevention of the various disorders described above. Using this approach, therapeutic efficacy with lower dosages of

each agent may be possible, thus reducing the potential for adverse side effects.

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including,
5 for example, mammals such as dogs, cats, cows, horses, rabbits, monkeys, and most preferably, humans.

Drug Screening

According to still another aspect of the invention,
10 nucleic acid molecules of the invention as well as peptides of the invention, particularly purified mutant ion channel subunit polypeptide and cells expressing these, are useful for the screening of candidate pharmaceutical agents for the treatment of epilepsy as
15 well as other as other disorders associated with ion channel dysfunction, including but not restricted to, hyper- or hypo-kalemic periodic paralysis, myotonias, malignant hyperthermia, myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's disease,
20 Parkinson's disease, schizophrenia, hyperekplexia, anxiety, depression, phobic obsessive symptoms, neuropathic pain, inflammatory pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease, Dent's disease, hyperinsulinemic hypoglycemia of infancy, cystic
25 fibrosis, congenital stationary night blindness or total colour-blindness.

Still further, it provides the use of a polypeptide complex for the screening of candidate pharmaceutical compounds.

30 Still further, it provides the use wherein high throughput screening techniques are employed.

Compounds that can be screened in accordance with the invention include, but are not limited to peptides (such as soluble peptides), phosphopeptides and small organic or
35 inorganic molecules (such as natural product or synthetic chemical libraries and peptidomimetics).

In one embodiment, a screening assay may include a cell-based assay utilising eukaryotic or prokaryotic host cells that are stably transformed with recombinant molecules expressing the polypeptides or fragments of the invention, in competitive binding assays. Binding assays will measure the formation of complexes between a specific mutant ion channel subunit polypeptide or ion channel incorporating a mutant ion channel subunit polypeptide, and the compound being tested, or will measure the degree to which a compound being tested will inhibit or restore the formation of a complex between a specific mutant ion channel subunit polypeptide or ion channel incorporating a mutant ion channel subunit polypeptide, and its interactor or ligand.

The invention is particularly useful for screening compounds by using the polypeptides of the invention in transformed cells, transfected or injected oocytes, or animal models bearing mutated ion channel subunits such as transgenic animals or gene targeted (knock-in) animals (see transformed hosts). Drug candidates can be added to cultured cells that express a single mutant ion channel subunit or combination of mutant ion channel subunits (appropriate wild-type ion channel subunits should also be expressed for receptor assembly), can be added to oocytes transfected or injected with either a mutant ion channel subunit or combination of mutant ion channel subunits (appropriate wild-type ion channel subunits must also be injected for receptor assembly), or can be administered to an animal model containing a mutant ion channel or combination of mutant ion channels. Determining the ability of the test compound to modulate mutant ion channel activity can be accomplished by a number of techniques known in the art. These include for example measuring the effect on the current of the channel (e.g. calcium-, chloride-, sodium-, potassium-ion flux) as compared to the current of a cell or animal containing wild-type ion channels. Current in cells can be measured

by a number of approaches including the patch-clamp technique (methods described in Hamill et al, 1981) or using fluorescence based assays as are known in the art (see Gonzalez et al. 1999). Drug candidates that alter the 5 current to a more normal level are useful for treating or preventing epilepsy as well as other disorders associated with ion channel dysfunction.

Non cell-based assays may also be used for identifying compounds that can inhibit or restore binding 10 between the polypeptides of the invention or ion channels incorporating the polypeptides of the invention, and their interactors. Such assays are known in the art and include for example AlphaScreen technology (PerkinElmer Life Sciences, MA, USA). This application relies on the use of 15 beads such that each interaction partner is bound to a separate bead via an antibody. Interaction of each partner will bring the beads into proximity, such that laser excitation initiates a number of chemical reactions ultimately leading to fluorophores emitting a light 20 signal. Candidate compounds that inhibit the binding of the mutant ion channel subunit, or ion channel incorporating the mutant subunit, with its interactor will result in loss of light emission, while candidate compounds that restore the binding of the mutant ion 25 channel subunit, or ion channel incorporating the mutant subunit, with its interactor will result in positive light emission. These assays ultimately enable identification and isolation of the candidate compounds.

High-throughput drug screening techniques may also 30 employ methods as described in WO84/03564. Small peptide test compounds synthesised on a solid substrate can be assayed for mutant ion channel subunit polypeptide or mutant ion channel binding. Bound mutant ion channel or 35 mutant ion channel subunit polypeptide is then detected by methods well known in the art. In a variation of this technique, purified polypeptides of the invention can be

coated directly onto plates to identify interacting test compounds.

The invention also contemplates the use of competition drug screening assays in which neutralizing antibodies capable of specifically binding the mutant ion channel compete with a test compound for binding thereto. In this manner, the antibodies can be used to detect the presence of any peptide that shares one or more antigenic determinants of the mutant ion channel.

The polypeptides of the present invention may also be used for screening compounds developed as a result of combinatorial library technology. This provides a way to test a large number of different substances for their ability to modulate activity of a polypeptide. A substance identified as a modulator of polypeptide function may be peptide or non-peptide in nature. Non-peptide "small molecules" are often preferred for many *in vivo* pharmaceutical applications. In addition, a mimic or mimetic of the substance may be designed for pharmaceutical use. The design of mimetics based on a known pharmaceutically active compound ("lead" compound) is a common approach to the development of novel pharmaceuticals. This is often desirable where the original active compound is difficult or expensive to synthesise or where it provides an unsuitable method of administration. In the design of a mimetic, particular parts of the original active compound that are important in determining the target property are identified. These parts or residues constituting the active region of the compound are known as its pharmacophore. Once found, the pharmacophore structure is modelled according to its physical properties using data from a range of sources including x-ray diffraction data and NMR. A template molecule is then selected onto which chemical groups which mimic the pharmacophore can be added. The selection can be made such that the mimetic is easy to synthesise, is likely to be pharmacologically acceptable, does not

degrade *in vivo* and retains the biological activity of the lead compound. Further optimisation or modification can be carried out to select one or more final mimetics useful for *in vivo* or clinical testing.

5 It is also possible to isolate a target-specific antibody and then solve its crystal structure. In principle, this approach yields a pharmacophore upon which subsequent drug design can be based as described above. It may be possible to avoid protein crystallography
10 altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analogue of the original receptor. The anti-id could then be used to
15 isolate peptides from chemically or biologically produced peptide banks.

Another alternative method for drug screening relies on structure-based rational drug design. Determination of the three dimensional structure of the polypeptides of the invention, or the three dimensional structure of the ion channels which incorporate these polypeptides allows for structure-based drug design to identify biologically active lead compounds.

Three dimensional structural models can be generated
25 by a number of applications, some of which include experimental models such as x-ray crystallography and NMR and/or from *in silico* studies of structural databases such as the Protein Databank (PDB). In addition, three dimensional structural models can be determined using a
30 number of known protein structure prediction techniques based on the primary sequences of the polypeptides (e.g. SYBYL - Tripos Associated, St. Louis, MO), *de novo* protein structure design programs (e.g. MODELER - MSI Inc., San Diego, CA, or MOE - Chemical Computing Group, Montreal,
35 Canada) or *ab initio* methods (e.g. see US Patent Numbers 5331573 and 5579250).

Once the three dimensional structure of a polypeptide or polypeptide complex has been determined, structure-based drug discovery techniques can be employed to design biologically-active compounds based on these three 5 dimensional structures. Such techniques are known in the art and include examples such as DOCK (University of California, San Francisco) or AUTODOCK (Scripps Research Institute, La Jolla, California). A computational docking protocol will identify the active site or sites that are 10 deemed important for protein activity based on a predicted protein model. Molecular databases, such as the Available Chemicals Directory (ACD) are then screened for molecules that complement the protein model.

Using methods such as these, potential clinical drug 15 candidates can be identified and computationally ranked in order to reduce the time and expense associated with typical 'wet lab' drug screening methodologies.

Compounds identified through screening procedures as described above, and which are based on the use of the 20 mutant nucleic acid and polypeptides of the invention, can also be tested for their effect on correcting the functional deficit imposed by other gene mutations in affected individuals including other ion channel subunit mutations.

Such compounds form a part of the present invention, 25 as do pharmaceutical compositions containing these and a pharmaceutically acceptable carrier.

Pharmaceutical Preparations

Compounds identified from screening assays and shown 30 to restore ion channel wild-type activity can be administered to a patient at a therapeutically effective dose to treat or ameliorate epilepsy as well as other disorders associated with ion channel dysfunction, as 35 described above. A therapeutically effective dose refers to that amount of the compound sufficient to result in amelioration of symptoms of the disorder.

Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals. The data obtained from these studies can then be used in the formulation of 5 a range of dosages for use in humans.

Pharmaceutical compositions for use in accordance with the present invention can be formulated in a conventional manner using one or more physiological acceptable carriers, excipients or stabilisers which are 10 well known. Acceptable carriers, excipients or stabilizers are non-toxic at the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) 15 polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; binding agents including hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates 20 including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or non-ionic surfactants such as Tween, Pluronics or polyethylene glycol (PEG).

The formulation of pharmaceutical compositions for 25 use in accordance with the present invention will be based on the proposed route of administration. Routes of administration may include, but are not limited to, inhalation, insufflation (either through the mouth or nose), oral, buccal, rectal or parental administration.

Diagnostic Applications

Polynucleotide sequences encoding an ion channel 35 subunit may be used for the diagnosis of epilepsy, as well as other disorders associated with ion channel dysfunction, including but not restricted to, hyper- or hypo-kalemic periodic paralysis, myotonias, malignant

hyperthermia, myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's disease, Parkinson's disease, schizophrenia, hyperekplexia, anxiety, depression, phobic obsessive symptoms, neuropathic pain, inflammatory pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease, Dent's disease, hyperinsulinemic hypoglycemia of infancy, cystic fibrosis, congenital stationary night blindness or total colour-blindness, and the use of the nucleic acid molecules incorporated as part of the invention in diagnosis of these disorders, or a predisposition to these disorders, is therefore contemplated. The nucleic acid molecules incorporating the novel mutation events laid out in Table 1 may be used for this purpose.

The polynucleotides that may be used for diagnostic purposes include oligonucleotide sequences, genomic DNA and complementary RNA and DNA molecules. The polynucleotides may be used to detect and quantitate gene expression in biological samples. Genomic DNA used for the diagnosis may be obtained from body cells, such as those present in the blood, tissue biopsy, surgical specimen, or autopsy material. The DNA may be isolated and used directly for detection of a specific sequence or may be amplified by the polymerase chain reaction (PCR) prior to analysis. Similarly, RNA or cDNA may also be used, with or without PCR amplification. To detect a specific nucleic acid sequence, hybridisation using specific oligonucleotides, restriction enzyme digest and mapping, PCR mapping, RNase protection, and various other methods may be employed. Oligonucleotides specific to particular sequences can be chemically synthesized and labelled radioactively or nonradioactively and hybridised to individual samples immobilized on membranes or other solid-supports or in solution. The presence, absence or excess expression of any one of the mutant ion channel genes of the invention may then be visualized using

methods such as autoradiography, fluorometry, or colorimetry.

In a further diagnostic approach, the nucleotide sequences of the invention may be useful in assays that detect the presence of associated disorders, particularly those mentioned previously. The nucleotide sequences may be labelled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridisation complexes. After a suitable incubation period, the sample is washed and the signal is quantitated and compared with a standard value. If the amount of signal in the patient sample is significantly altered in comparison to a control sample then the presence of altered levels of nucleotide sequences in the sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

In order to provide a basis for the diagnosis or prognosis of epilepsy and other disorders as described above, which are associated with the ion channel subunit mutations or variants of the invention, the nucleotide sequence of each gene can be compared between normal tissue and diseased tissue in order to establish whether the patient expresses a mutant gene.

In order to provide a basis for the diagnosis of a disorder associated with abnormal expression of an ion channel subunit gene of the invention, a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, encoding the relevant ion channel subunit gene, under conditions suitable for hybridisation or amplification. Standard hybridisation may be quantified by comparing the values obtained from normal subjects with values from an experiment in which a known

amount of a substantially purified polynucleotide is used. Another method to identify a normal or standard profile for expression of an ion channel subunit gene is through quantitative RT-PCR studies. RNA isolated from body cells 5 of a normal individual is reverse transcribed and real-time PCR using oligonucleotides specific for the relevant gene is conducted to establish a normal level of expression of the gene. Standard values obtained in both these examples may be compared with values obtained from 10 samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder.

Once the presence of a disorder is established and a treatment protocol is initiated, hybridisation assays or 15 quantitative RT-PCR studies may be repeated on a regular basis to determine if the level of expression in the patient begins to approximate that which is observed in the normal subject. The results obtained from successive assays may be used to show the efficacy of treatment over 20 a period ranging from several days to months.

According to a further aspect of the invention there is provided the use of a polypeptide as described above in the diagnosis of epilepsy as well as other disorders associated with ion channel dysfunction, including but not 25 restricted to, hyper- or hypo-kalemic periodic paralysis, myotonias, malignant hyperthermia, myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's disease, Parkinson's disease, schizophrenia, hyperekplexia, anxiety, depression, phobic obsessive 30 symptoms, neuropathic pain, inflammatory pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease, Dent's disease, hyperinsulinemic hypoglycemia of infancy, cystic fibrosis, congenital stationary night blindness or total colour-blindness.

35 When a diagnostic assay is to be based upon proteins constituting an ion channel, a variety of approaches are possible. For example, diagnosis can be achieved by

monitoring differences in the electrophoretic mobility of normal and mutant proteins that form the ion channel. Such an approach will be particularly useful in identifying mutants in which charge substitutions are present, or in
5 which insertions, deletions or substitutions have resulted in a significant change in the electrophoretic migration of the resultant protein. Alternatively, diagnosis may be based upon differences in the proteolytic cleavage patterns of normal and mutant proteins, differences in
10 molar ratios of the various amino acid residues, or by functional assays demonstrating altered function of the gene products.

In another aspect, antibodies that specifically bind mutant ion channels may be used for the diagnosis of a disorder, or in assays to monitor patients being treated with a complete ion channel or agonists, antagonists, modulators or inhibitors of an ion channel. Antibodies useful for diagnostic purposes may be prepared in the same manner as described above for therapeutics. Diagnostic
15 assays for ion channels include methods that utilize the antibody and a label to detect a mutant ion channel in human body fluids or in extracts of cells or tissues. The antibodies may be used with or without modification, and may be labelled by covalent or non-covalent attachment of
20 a reporter molecule.
25

A variety of protocols for measuring the presence of mutant ion channels, including but not restricted to, ELISAs, RIAs, and FACS, are known in the art and provide a basis for diagnosing a disorder. The expression of a
30 mutant ion channel or combination of mutant ion channels is established by combining body fluids or cell extracts taken from test mammalian subjects, preferably human, with antibody to the ion channel or channels under conditions suitable for complex formation. The amount of complex
35 formation may be quantitated by various methods, preferably by photometric means. Antibodies specific for the mutant ion channels will only bind to individuals

expressing the said mutant ion channels and not to individuals expressing only wild-type channels (ie normal individuals). This establishes the basis for diagnosing the disorder.

5 Once an individual has been diagnosed with a disorder, effective treatments can be initiated as described above. Treatments can be directed to amend the combination of ion channel subunit mutations or may be directed to one mutation.

10

Microarray

In further embodiments, complete cDNAs, oligonucleotides or longer fragments derived from any of the polynucleotide sequences described herein may be used 15 as probes in a microarray. The microarray can be used to diagnose epilepsy, as well as other disorders associated with ion channel dysfunction, through the identification of genetic variants, mutations, and polymorphisms in the ion channel subunits that form part of the invention, to 20 understand the genetic basis of a disorder, or can be used to develop and monitor the activities of therapeutic agents.

According to a further aspect of the present invention, tissue material obtained from animal models 25 generated as a result of the identification of specific ion channel subunit human mutations (see below), particularly those disclosed in the present invention, can be used in microarray experiments. These experiments can be conducted to identify the level of expression of 30 specific ion channel subunits, or any cDNA clones from whole-tissue libraries, in diseased tissue as opposed to normal control tissue. Variations in the expression level of genes, including ion channel subunits, between the two tissues indicates their possible involvement in the 35 disease process either as a cause or consequence of the original ion channel subunit mutation present in the animal model. These experiments may be used to determine

gene function, to understand the genetic basis of a disorder, to diagnose a disorder, and to develop and monitor the activities of therapeutic agents. Microarrays may be prepared, used, and analyzed using methods known in
5 the art. (For example, see Schena et al., 1996; Heller et al., 1997).

Transformed Hosts

The present invention also provides for the
10 production of genetically modified (knock-out, knock-in and transgenic), non-human animal models transformed with nucleic acid molecules containing the novel ion channel mutations or variants as laid out in Table 1. These animals are useful for the study of the function of ion
15 channels, to study the mechanisms by which combinations of mutations in ion channel subunits interact to give rise to disease and the effects of these mutations on tissue development, for the screening of candidate pharmaceutical compounds, for the creation of explanted mammalian cell
20 cultures which express mutant ion channels or combinations of mutant ion channels, and for the evaluation of potential therapeutic interventions.

Animal species which are suitable for use in the animal models of the present invention include, but are not limited to, rats, mice, hamsters, guinea pigs, rabbits, dogs, cats, goats, sheep, pigs, and non-human primates such as monkeys and chimpanzees. For initial studies, genetically modified mice and rats are highly desirable due to the relative ease in generating knock-in, knock-out or transgenics of these animals, their ease of maintenance and their shorter life spans. For certain studies, transgenic yeast or invertebrates may be suitable and preferred because they allow for rapid screening and provide for much easier handling. For longer term studies, 35 non-human primates may be desired due to their similarity with humans.

To create an animal model for a mutated ion channel, or an animal model incorporating a combination of mutations, several methods can be employed. These include, but are not limited to, generation of a specific mutation 5 in a homologous animal gene, insertion of a wild type human gene and/or a humanized animal gene by homologous recombination, insertion of a mutant (single or multiple) human gene as genomic or minigene cDNA constructs using wild type or mutant or artificial promoter elements, or 10 insertion of artificially modified fragments of the endogenous gene by homologous recombination. The modifications include insertion of mutant stop codons, the deletion of DNA sequences, or the inclusion of recombination elements (lox p sites) recognized by enzymes 15 such as Cre recombinase.

To create transgenic mice in order to study gain of gene function *in vivo*, any mutant ion channel subunit gene of the invention can be inserted into a mouse germ line using standard techniques such as oocyte microinjection. 20 Gain of gene function can mean the over-expression of a gene and its protein product, or the genetic complementation of a mutation of the gene under investigation. For oocyte injection, one or more copies of the mutant gene can be inserted into the pronucleus of a 25 just-fertilized mouse oocyte. This oocyte is then reimplanted into a pseudo-pregnant foster mother. The live-born mice can then be screened for integrants using analysis of tail DNA for the presence of the relevant human ion channel subunit gene sequence. The transgene can 30 be either a complete genomic sequence injected as a YAC, BAC, PAC or other chromosome DNA fragment, a cDNA with either the natural promoter or a heterologous promoter, or a minigene containing all of the coding region and other elements found to be necessary for optimum expression.

35 To generate knock-out mice or knock-in mice, gene targeting through homologous recombination in mouse embryonic stem (ES) cells may be applied. Knock-out mice

are generated to study loss of gene function *in vivo* while knock-in mice (which are preferred) allow the study of gain of function or to study the effect of specific gene mutations. Knock-in mice are similar to transgenic mice
5 however the integration site and copy number are defined in the former.

For knock-out mouse generation, gene targeting vectors can be designed such that they delete (knock-out) the protein coding sequence of the relevant ion channel
10 subunit gene in the mouse genome. In contrast, knock-in mice can be produced whereby a gene targeting vector containing the relevant ion channel subunit gene can integrate into a defined genetic locus in the mouse genome. For both applications, homologous recombination is
15 catalysed by specific DNA repair enzymes that recognise homologous DNA sequences and exchange them via double crossover.

Gene targeting vectors are usually introduced into ES cells using electroporation. ES cell integrants are then
20 isolated via an antibiotic resistance gene present on the targeting vector and are subsequently genotyped to identify those ES cell clones in which the gene under investigation has integrated into the locus of interest. The appropriate ES cells are then transmitted through the
25 germline to produce a novel mouse strain.

In instances where gene ablation results in early embryonic lethality, conditional gene targeting may be employed. This allows genes to be deleted in a temporally and spatially controlled fashion. As above, appropriate ES cells are transmitted through the germline to produce a novel mouse strain, however the actual deletion of the
30 gene is performed in the adult mouse in a tissue specific or time controlled manner. Conditional gene targeting is most commonly achieved by use of the cre/lox system. The
35 enzyme cre is able to recognise the 34 base pair loxP sequence such that loxP flanked (or floxed) DNA is recognised and excised by cre. Tissue specific cre

expression in transgenic mice enables the generation of tissue specific knock-out mice by mating gene targeted floxed mice with cre transgenic mice. Knock-out can be conducted in every tissue (Schwenk et al., 1995) using the 'deleter' mouse or using transgenic mice with an inducible cre gene (such as those with tetracycline inducible cre genes), or knock-out can be tissue specific for example through the use of the CD19-cre mouse (Rickert et al., 1997).

Once knock-in animals have been produced which contain a specific mutation in a particular ion channel subunit, mating combinations may be initiated between such animals so as to produce progeny containing combinations of two or more ion channel mutations. These animals effectively mimic combinations of mutations that are proposed to cause human IGE cases. These animal models can subsequently be used to study the extent and mechanisms of disease as related to the mutated ion channel combinations, as well as for the screening of candidate therapeutic compounds.

According to still another aspect of the invention there is provided the use of genetically modified non-human animals as described above for the screening of candidate pharmaceutical compounds (see drug screening above). These animals are also useful for the evaluation (eg therapeutic efficacy, toxicity, metabolism) of candidate pharmaceutical compounds, including those identified from the invention as described above, for the treatment of epilepsy as well as other as other disorders associated with ion channel dysfunction as described above.

It will be clearly understood that, although a number of prior art publications are referred to herein, this reference does not constitute an admission that any of these documents forms part of the common general knowledge in the art, in Australia or in any other country.

Throughout this specification and the claims, the

words "comprise", "comprises" and "comprising" are used in a non-exclusive sense, except where the context requires otherwise.

It will be apparent to the person skilled in the art
5 that while the invention has been described in some detail
for the purposes of clarity and understanding, various
modifications and alterations to the embodiments and
methods described herein may be made without departing
from the scope of the inventive concept disclosed in this
10 specification.

Brief Description of the Drawings

Preferred forms of the invention will now be described, by way of example only, with reference to the
15 following examples and the accompanying drawings, in which:

Figure 1 provides an example of ion channel subunit stoichiometry and the effect of multiple versus single ion channel subunit mutations. Figure 1A: A typical channel
20 may have five subunits of three different types. Figure 1B: In outbred populations complex diseases such as idiopathic generalized epilepsies may be due to mutations in two (or more) different subunit genes. Because only one allele of each subunit gene is abnormal, half the
25 expressed subunits will have the mutation. Figure 1C: In inbred populations, both alleles of a single subunit gene will be affected, so all expressed subunits will be mutated. Figure 1D: Autosomal dominant disorders can be attributed to single ion channel subunit mutations that
30 give rise to severe functional consequences.

Figure 2 represents the location of mutations identified in the KCNQ2 ion channel subunit constituting the potassium channel. M: Missense mutation; T: Truncation mutation; F: Frameshift mutation; S: Splice site mutation.

35 Figure 3 provides examples of epilepsy pedigrees where mutation profiles of ion channel subunits for individuals constituting the pedigree have begun to be

determined. These examples have been used to illustrate how the identification of novel ion channel subunit mutations and variations in IGE individuals can combine to give rise to the disorder.

5 Figure 4 shows the results of yeast two-hybrid analysis of R353G and L619R KCNQ2 mutants. Yeast were transformed with the empty DB (BAIT) plasmid (DBLeu), DB-Q2C wt, DB-Q2C R353G mutant or the DB-Q2 L619R mutant as indicated in A and the AD-CaM (TARGET) vector was
10 introduced by gap-repair. Yeast control strains (Invitrogen™) were included on all plates for comparison. Control 1 has no interaction. Control 2 has a weak interaction. Control 3 has a moderately strong interaction. Control 4 has a strong interaction and
15 control 5 has a very strong interaction. B. Growth of transformed yeast and controls on -leu -tryp selection. Yeast can grow on -leu if they contain the DB plasmid, and -tryp if they have AD plasmid. C. Growth of transformed yeast and controls on -leu -tryp -his +40mM 3AT after
20 48hrs. Yeast can grow on -his+3AT if the his reporter gene is activated by interaction between the BAIT and TARGET plasmids. D-F. LacZ Filter assay for interaction between BAIT and TARGET plasmids, photos taken after 2hrs (D), 7hrs (E) and 24hrs (F). Activation of the β -galactosidase reporter gene by interaction of the BAIT and TARGET plasmids leads to the dark appearance of colonies.
25

Figure 5 shows the results of CaM affinity experiments with the R353G and L619R KCNQ2 mutants. The chart below shows the values from the CPRG assay for β -galactosidase activity as a measure of KCNQ2C-CaM binding efficiency. The area of each bar in the chart equates to the CaM binding efficiency of the BAIT. Broken lines indicate statistical comparison by Student's t test. *
30 P<0.01, ** P<0.001.

Modes for Performing the Invention

Potassium channels are the most diverse class of ion channel. The *C. elegans* genome encodes about 80 different potassium channel genes and there are probably more in mammals. About ten potassium channel genes are known to be mutated in human disease and include four members of the KCNQ gene sub-family of potassium channels. KCNQ proteins have six transmembrane domains, a single P-loop that forms the selectivity filter of the pore, a positively charged fourth transmembrane domain that probably acts as a voltage sensor, and intracellular amino and carboxy termini. The C-terminus is long and contains a conserved "A domain" followed by a short stretch thought to be involved in subunit assembly.

Four KCNQ subunits are thought to combine to form a functional potassium channel. All five known KCNQ proteins can form homomeric channels *in vitro* and the formation of heteromers appears to be restricted to certain combinations. For instance KCNQ2 and KCNQ3, which are predominantly expressed in the central nervous system, form a heteromultimeric channel that mediates the neuronal muscarinic-regulated current (M-current), also known as the M-channel (or M-type K⁺ channel). The M-current is a slowly activating, non-inactivating potassium conductance known to regulate neuronal excitability by determining the firing properties of neurons and their responsiveness to synaptic input (Wang et al., 1998). Because it is the only current active at voltages near the threshold for action potential initiation, the M-current has a major impact on neuronal excitability.

Sodium (the alpha subunit) and calcium channels are thought to have evolved from the potassium channel subunit, and they each consist of four domains covalently linked as the one molecule, each domain being equivalent to one of the subunits that associate to form the potassium channel. Each of the four domains of the sodium and calcium channels are comprised of six transmembrane

segments.

Voltage-gated sodium channels are required to generate the electrical excitation in neurones, heart and skeletal muscle fibres, which express tissue specific isoforms. Sodium channels are heteromers of a pore forming alpha subunit and a modulatory beta-1 subunit, with an additional beta-2 subunit in neuronal channels. Ten genes encoding sodium channel alpha subunits and 3 genes encoding different beta subunits have so far been identified. The beta subunits of the sodium channels do not associate with the alpha subunits to form any part of the pore, they do however affect the way the alpha pore forming subunit functions.

As with sodium channels, calcium channels consist of a single pore forming alpha subunit, of which at least six types have been identified to date, and several accessory subunits including four beta, one gamma and one alpha-delta gene. Many of these subunits also encode multiple splice variants adding to the diversity of receptor subunits of this family of ion channels.

The ion channels in the nAChR/GABA super family show a theoretical pentameric channel. Gamma-Aminobutyric acid (GABA) is the most abundant inhibitory neurotransmitter in the central nervous system. GABA-ergic inhibition is mediated by two major classes of receptors, type A (GABA-A) and type B (GABA-B). GABA-B receptors are members of the class of receptors coupled to G-proteins and mediate a variety of inhibitory effects via secondary messenger cascades. GABA-A receptors are ligand-gated chloride channels that mediate rapid inhibition.

The GABA-A channel has 16 separate, but related, genes encoding subunits. These are grouped on the basis of sequence identity into alpha, beta, gamma, delta, epsilon, theta and pi subunits. There are six alpha subunits ($\alpha 1-\alpha 6$), three beta subunits ($\beta 1-\beta 3$) and three gamma subunits ($\gamma 1-\gamma 3$). Each GABA-A receptor comprises five subunits which may, at least in theory, be selected from any of these

subunits.

Neuronal nicotinic acetylcholine receptors (nAChRs) consist of heterologous pentamers comprising various combinations of alpha subunits or alpha and beta subunits (α₂-α₉; β₂-β₄). The alpha subunits are characterised by adjacent cysteine residues at amino acid positions 192 and 193, and the beta subunits by the lack of these cysteine residues. They are ligand-gated ion channels differentially expressed throughout the brain to form physiologically and pharmacologically distinct receptors hypothesised to mediate fast, excitatory transmission between neurons of the central nervous system or to modulate neurotransmission from their presynaptic position.

In chicken and rat, the predominant nAChR subtype is composed of alpha-4 and beta-2 subunits. The transmembrane 2 (M2) segments of the subunits are arranged as alpha helices and contribute to the walls of the neurotransmitter-gated ion channel. The alpha helices appear to be kinked and orientated in such a way that the side chains of the highly conserved M2-leucine residues project inwards when the channel is closed. ACh is thought to cause a conformational change by altering the association of the amino acid residues of M2. The opening of the channel seems to be due to rotations of the gate forming side chains of the amino acid residues; the conserved polar serines and threonines may form the critical gate in the open channel.

Example 1: Identification of mutations in ion channels

Previous studies by reference (Wallace et al., 1998; PCT/AU01/00581; Wallace et al., 2001b; Australian patent AU-B-56247/96; Steinlein et al., 1995; PCT/AU01/00541; Phillips et al., 2001; PCT/AU01/00729; PCT/AU01/01648; PCT/AU02/00910; Wallace et al., 2001a, the disclosures of which are incorporated herein by reference) have identified mutations in a number of ion channel subunits

associated with epilepsy. These include ion channel subunits of voltage-gated (eg SCN1A, SCN1B, KCNQ2, KCNQ3) or ligand-gated (eg CHRNA4, CHRNB2, GABRG2, GABRD) types. To identify further mutations in ion channel genes, 5 subunits which comprise the ion channels were screened for molecular defects in epilepsy patients.

Human genomic sequence available from the Human Genome Project was used to characterize the genomic organisation for each subunit gene. Each gene was 10 subsequently screened for sequence changes using single strand conformation polymorphism (SSCP) analysis in a large sample of epileptics with common sporadic IGE subtypes eg juvenile myoclonic epilepsy (JME), childhood absence epilepsy (CAE), juvenile absence epilepsy (JAE) 15 and epilepsy with generalized tonic-clonic seizures (TCS). Clinical observations can then be compared to the molecular defects characterized in order to establish the combinations of mutant subunits involved in the various disease states, and therefore to provide validated drug 20 targets for each of these disease states. This will provide a basis for novel drug treatments directed at the genetic defects present in each patient.

The coding sequence for each of the ion channel subunits was aligned with human genomic sequence present 25 in available databases at the National Centre for Biotechnology Information (NCBI). The BLASTN algorithm was typically used for sequence alignment and resulted in the genomic organisation (intron-exon structure) of each gene being determined. Where genomic sequence for an ion 30 channel subunit was not available, BACs or PACs containing the relevant ion channel subunit were identified through screening of high density filters containing these clones and were subsequently sequenced.

Availability of entire genomic sequence for each ion 35 channel subunit facilitated the design of intronic primers spanning each exon. These primers were used for both high throughput SSCP screening and direct DNA sequencing.

Example 2: Sample preparation for SSCP screening

A large collection of individuals affected with epilepsy have undergone careful clinical phenotyping and additional data regarding their family history has been collated. Informed consent was obtained from each individual for blood collection and its use in subsequent experimental procedures. Clinical phenotypes incorporated classical IGE cases as well as GEFS+ and febrile seizure cases.

DNA was extracted from collected blood using the QIAamp DNA Blood Maxi kit (Qiagen) according to manufacturers specifications or through procedures adapted from Wyman and White (1980). Stock DNA samples were kept at a concentration of 1 ug/ μ l.

In preparation for SSCP analysis, samples to be screened were formatted into 96-well plates at a concentration of 30 ng/ μ l. These master plates were subsequently used to prepare exon specific PCR reactions in the 96-well format.

Example 3: Identification of sequence alterations in ion channel genes

SSCP analysis of specific ion channel exons followed by sequencing of SSCP bandshifts was performed on individuals constituting the 96-well plates to identify sequence alterations.

Primers used for SSCP were labelled at their 5' end with HEX and typical PCR reactions were performed in a total volume of 10 μ l. All PCR reactions contained 67 mM Tris-HCl (pH 8.8); 16.5 mM $(\text{NH}_4)_2\text{SO}_4$; 6.5 μ M EDTA; 1.5 mM MgCl₂; 200 μ M each dNTP; 10% DMSO; 0.17 mg/ml BSA; 10 mM β -mercaptoethanol; 5 μ g/ml each primer and 100 U/ml Tag DNA polymerase. PCR reactions were performed using 10 cycles of 94°C for 30 seconds, 60°C for 30 seconds, and 72°C for 30 seconds followed by 25 cycles of 94°C for 30 seconds, 55°C for 30 seconds, and 72°C for 30 seconds. A final

extension reaction for 10 minutes at 72°C followed.

Twenty μ l of loading dye comprising 50% (v/v) formamide, 12.5 mM EDTA and 0.02% (w/v) bromophenol blue were added to completed reactions which were subsequently 5 run on non-denaturing 4% polyacrylamide gels with a cross-linking ratio of 35:1 (acrylamide:bis-acrylamide) and containing 2% glycerol. Gel thickness was 100 μ m, width 168mm and length 160mm. Gels were run at 1200 volts and approximately 20mA, at 22°C and analysed on the GelScan 10 2000 system (Corbett Research, Australia) according to manufacturers specifications.

PCR products showing a conformational change were subsequently sequenced. This first involved re-amplification of the amplicon from the relevant individual 15 (primers used in this instance did not contain 5' HEX labels) followed by purification of the PCR amplified templates for sequencing using QiaQuick PCR preps (Qiagen) based on manufacturers procedures. The primers used to sequence the purified amplicons were identical to those 20 used for the initial amplification step. For each sequencing reaction, 25 ng of primer and 100 ng of purified PCR template were used. The BigDye sequencing kit (ABI) was used for all sequencing reactions according to the manufacturers specifications. The products were run on 25 an ABI 377 Sequencer and analysed using the EditView program.

Table 1 shows the novel sequence changes identified in the ion channel subunits screened.

30 Example 4: Digenic model examples

In some instances a single mutation in an ion channel alone is insufficient to give rise to an epilepsy phenotype. However combinations of mutations each conferring a subtle change of function to an ion channel, 35 as proposed by the digenic model (PCT/AU01/00872), may be sufficient to produce an epilepsy phenotype.

Using the mutations and variations in ion channel

subunits that form part of this invention, the digenic model may be validated through a parametric analysis of large families in which two abnormal alleles co-segregate by chance to identify mutations which act co-operatively 5 to give an epilepsy phenotype. It is envisaged that the strategy of careful clinical phenotyping in these large families, together with a linkage analysis based on the digenic hypothesis will allow identification of the mutations in ion channels associated with IGEs. If 10 molecular genetic studies in IGE are successful using the digenic hypothesis, such an approach might serve as a model for other disorders with complex inheritance.

The digenic hypothesis predicts that the closer the genetic relationship between affected individuals, the 15 more similar the sub-syndromes, consistent with published data (Italian League Against Epilepsy Genetic Collaborative Group, 1993). This is because more distant relatives are less likely to share the same combinations of mutated subunits.

20 Identical twins have the same pair of mutated subunits and the same minor alleles so the sub-syndromes are identical. Affected sib-pairs, including dizygous twins, with the same sub-syndrome would also have the same pair of mutated subunits, but differences in minor alleles 25 would lead to less similarity than with monozygous twins. Some sib-pairs and dizygous twins, have quite different sub-syndromes; this would be due to different combinations of mutated subunits, when the parents have more than two mutated alleles between them.

30 A special situation exists in inbred communities that parallels observations on autosomal recessive mouse models. Here the two mutated alleles of the digenic model are the same and thus result in a true autosomal recessive disorder. Because all affected individuals have the same 35 pair of mutated alleles, and a similar genetic background, the phenotypes are very similar.

In outbred communities approximately 1% of the

population would have IGE genotypes (2 mutated alleles) and 0.3% would clinically express IGE. Most of these would have mutations in two different channel subunits. In such communities most cases would appear "sporadic" as the risk 5 to first degree relatives would be less than 10%.

For example, let there be three IGE loci (A,B,C) and let the frequency of abnormal alleles (a^*, b^*, c^*) at each locus be .027 and of normal alleles (a, b, c) be .973. Then, the distribution of genotypes aa^* , a^*a , a^*a^* and aa 10 at locus A will be .0263 (.027 x .973), .0263, .0007 and .9467 respectively, and similarly for loci B and C. In this population .8485 will have no mutated alleles (.9467³), .1413 will have one mutated allele (a* or b* or c*; .0263 x .9467² x 6), .0098 will have two abnormal 15 alleles (.0020 two same abnormal alleles, .0078, two different abnormal alleles) and 0.00037 will have more than two abnormal alleles. Thus in this population .01, or 1%, will have two or more abnormal alleles (IGE genotype), and the total abnormal allele frequency will be .08 (3 x 20 .027).

To determine the familial risks and allele patterns in affected pairs, the frequency distribution of population matings and the percentage of children with 2 or more abnormal alleles must be determined. The frequency 25 of matings with no abnormal alleles (0 x 0) is .72 (.8485²), for 1 x 0 and 0 x 1 matings .24 (2 x .8485 x .1413), for a 1 x 1 mating .020, and for 2 x 0 and 0 x 2 matings .0166 etc. From this distribution of matings the frequency of children with 2 or more abnormal alleles can 30 be shown to be .01. For example, the 0 x 2 and 2 x 0 matings contribute .0033 of this .01 frequency (.0166 [mating frequency] x .2 [chance of that mating producing a child with 2 or more abnormal alleles]).

To determine parental risk it can be shown that of 35 children with 2 abnormal alleles (IGE genotype), .49 derive from 1 x 1 matings where no parent is affected, .33 derive from a 2 x 0 and 0 x 2 matings etc. For the 2 x 0

and 0×2 matings, half the parents have IGE genotypes and contribute .16 (.33/2) to the parental risk with the total parental risk of an IGE genotype being .258. The other matings that contribute to affected parent-child pairs are
5 2×1 , 1×2 , 3×0 , 0×3 etc.

The sibling risk of an IGE genotype is .305. For example 2×0 and 0×2 matings contributed .08 to the sibling risk (.33[fraction of children with 2 abnormal alleles] \times .25[the chance of that mating producing a child
10 with 2 or more abnormal alleles]). Similarly the offspring risk was determined to be .248 by mating individuals with 2 abnormal alleles with the general population. Thus at 30% penetrance the risk for IGE phenotype for parents of a proband is .077, for siblings .091, and for offspring
15 .074.

It can be shown that affected sib pairs share the same abnormal allele pair in 85% of cases. This is because of all affected sib pairs 44% derive from 1×1 matings and 23% from 0×2 and 2×0 matings where all affected
20 siblings have the same genotype. In contrast, 24% derive from 1×2 matings and 9% from 3×1 and 2×2 matings etc where affected sibling genotypes sometimes differ.

For affected parent-child pairs, genotypes are identical in only 58%. Of affected parent child pairs, 43%
25 derive from 0×2 matings where gentotypes are identical, whereas 38% derive from 0×3 and 17% from 1×2 where the majority of crosses yield different affected genotypes.

Based on the digenic model it has been postulated that most classical IGE and GEFS' cases are due to the
30 combination of two mutations in multi-subunit ion channels. These are typically point mutations resulting in a subtle change of function. The critical postulate is that two mutations, usually, but not exclusively, in different subunit alleles ("digenic model"), are required
35 for clinical expression of IGE.

The hypothesis that similar phenotypes can be caused by the combination of mutations in two (or more) different

subunits (outbred communities), or by the same mutation in two (or more) alleles of the same subunit (inbred communities), may seem implausible. However, applying the digenic hypothesis to the theoretical pentameric channel shown in Figure 1, in outbred communities IGE will be due to subunit combinations such as $\alpha^*\alpha\beta^*\beta\Delta$, $\alpha^*\alpha\beta\beta\Delta^*$ or $\alpha\alpha\beta^*\beta\Delta^*$ (mutated subunits indicated by *). In inbred communities $\alpha^*\alpha^*\beta\beta\Delta$ or $\alpha\alpha\beta^*\beta^*\Delta$ combinations might cause IGE phenotypes. We assume that the mutations will not cause reduced expression of the alleles and that the altered ion channel excitability, and consequent IGE phenotype, caused by mutations in two different alleles is similar to that caused by the same mutation in both alleles of one subunit. Finally, subunit mutations with more severe functional consequences (eg breaking a disulphide bridge in SCN1B or amino acid substitution in the pore forming regions of SCN1A for GEFS⁺) cause autosomal dominant generalized epilepsies with a penetrance of 60-90%. Such "severe" mutations are rare (allele frequency <0.01%) and are infrequent causes of GEFS⁺. They very rarely, or perhaps never, cause classical IGE.

The relative separate segregation of classical IGE and GEFS⁺ phenotypes is an anecdotal clinical observation of ours (Singh et al., 1999), although the separation is not absolute. The separation is supported by previous family and EEG studies of Doose and colleagues who described "type A" and "type B" liabilities which we may approximate the GEFS⁺ and classical IGE groupings respectively (Doose and Baier, 1987).

The digenic model predicts that affected sib pairs will share the same genes in 85% of cases whereas they will have at least one different allele in the remaining 15%. In contrast, only 58% of parent-child pairs share the same alleles in a 3 locus model. Thus there should be greater similarity of syndromes between sibling pairs than parent-child pairs. This would be most objectively measured by age of onset and seizure types.

Estimates for the risk of febrile seizures or IGE in relatives vary. The estimates range from 5%-10% for siblings, 4%-6% for offspring, 3%-6% for parents, and 2-3% for grandparents. Underestimation may occur because IGE manifest in youth, and parents and particularly grandparents may be unaware of seizures in themselves in younger years. This is particularly true where there was stigma associated with epilepsy and where the epilepsy may have been mild and unrecognized. Underestimation of sibling and offspring risks occurs when unaffected young children are counted, some of whom will develop IGE in adolescence. Overestimation may occur with misdiagnosis of seizures or inclusion of seizures unrelated to IGE (e.g. due to trauma or tumors)

In autosomal dominant models the risk to affected relatives reduces proportionally (50% for first degree relatives, 25% for second degree etc). For all oligogenic or polygenic models the risk decreases more quickly. For a digenic model with three loci, the risks are 9.1% for siblings, 7.4% for offspring, 7.7% for parents. Rigorous measurement of the familial recurrence rates, with careful phenotyping and age-corrected risk estimates could be compared with the predictions from the digenic model, and it is proposed to do this.

There is a small amount of information on IGE families regarding haplotype distribution. For example, there is some evidence for a locus on 8q as determined by parametric linkage in a single family (Fong et al., 1998) and by non-parametric analysis in multiple small families (Zara et al., 1995). Interestingly, in the latter study the 8q haplotype not infrequently came from the unaffected parent. This would be quite compatible with the digenic model and evaluation of other data sets in this manner could be used to test the hypothesis, and it is proposed to do this.

Following the analysis of one large family with epilepsy where the two main phenotypes were childhood

absence epilepsy (CAE) and febrile seizures (FS), the inheritance of FS was found to be autosomal dominant and the penetrance 75%. However the inheritance of CAE in this family was not simple Mendelian, but suggestive of complex inheritance with the involvement of more than one gene. The power of this large family was used to explore the complex genetics of CAE further.

Linkage analysis on this family in which individuals with CAE, FS and FS+ were deemed affected led to the detection of linkage on chromosome 5q and identification of a mutation in the GABRG2 gene (R43Q) which is localised to this region (Wallace et al., 2001a; PCT/AU01/00729). All 10 tested individuals with FS alone in this family had this mutation and 7 CAE affected individuals in this family also had the mutation. To test the digenic model of IGEs in the CAE affected individuals, the whole genome screen of this family was reanalysed with only individuals with CAE considered affected. Linkage analysis was performed using FASTLINK v4.0, two-point lod scores were calculated assuming 50% penetrance and a 2% phenocopy rate and individuals with FS or FS+ were coded as unknown. Markers producing a lod score greater than 1 were reanalysed without a phenocopy rate and at the observed penetrance for CAE in this family (30%). Results from the analysis revealed significant linkage to chromosome 14q22-q23 (lod 3.4). This provides strong evidence for a second locus segregating with CAE affected individuals in this family. While the GABRG2 mutation is sufficient to cause FS, the CAE phenotype is thought to be due to both the GABRG2 mutation and a mutation occurring in a gene mapping to the 14q locus, as proposed by the digenic model.

For the application of the digenic model to sporadic cases of IGE and affected individuals belonging to smaller families in which genotyping and linkage analysis is not a feasible approach to disease gene identification, direct mutation analysis of ion channel genes in these individuals has been carried out as described above. In

Table 1 there is provided an indication of novel genetic alterations so far identified through mutation analysis screening of these individuals. Figure 2 provides an example to indicate where some of these mutations have occurred with respect to the potassium channel KCNQ2 gene.

The identification of novel mutations and variations in ion channel subunits in IGE individuals provides resources to further test the digenic hypothesis and mutation profiles are starting to accumulate for a number of subunit changes that are observed in the same individuals. Figure 3 provides results from some of these profiles.

Figure 3A shows a 3 generation family in which individual III-1 has myoclonic astatic epilepsy and contains a N43del mutation in the SCN3A gene as well as an A1067T mutation in the SCN1A gene. Individual I-1 also has the SCN3A mutation but alone this mutation is not sufficient to cause epilepsy in this individual. The SCN3A mutation has likely been inherited from the grandfather through the mother, while the SCN1A mutation is likely to arise from the father. Both parents are unaffected but have yet to be screened for the presence of the mutations in these subunits. Individual II-1 is likely to contain an as yet unidentified ion channel subunit mutation acting in co-operation with the SCN3A mutation already identified in this individual.

Figure 3B is another 3 generation family in which individual III-1 has myoclonic astatic epilepsy due to a combination of the same SCN3A and SCN1A mutations as above. However, in this family both parents have febrile seizures most likely due to the presence of just one of the mutations in each parent, as proposed by the model. This is in contrast to individuals II-2 and II-3 in Figure 4A who also contain one of the mutations in these genes each. These individuals are phenotypically normal most likely due to incomplete penetrance of these mutations in each case.

Figure 3C shows a larger multi-generation family in which individual IV-5 has a mutation in both the SCN3A and GABRG2 subunits. In combination, these give rise to severe myoclonic epilepsy of infancy but alone either cause
5 febrile seizures (GABRG2 mutation in III-3 and IV-4) or are without an effect (SCN3A mutation in III-2) as proposed by the model.

These examples therefore illustrate the digenic model as determined from mutation analysis studies of ion
10 channel subunits in affected individuals and highlight the need to identify genetic alterations in the genes encoding ion channel subunits.

Example 5: Analysis of ion channels and ion channel
15 subunits

The structure and function of the mutant ion channels and mutant ion channel subunits of the present invention can be determined using a variety of molecular biological studies. These studies may provide clues as to the
20 mechanisms by which mutations in ion channel subunits effect the functioning of the ion channel. For instance the identification of proteins that interact with mutant ion channels (or whose interaction is impeded by a mutation in an ion channel subunit) may help determine the
25 molecular mechanisms that are disrupted as a result of a mutation. Procedures such as the yeast two-hybrid system can be used to discover and identify such interacting proteins.

The principle behind the yeast two-hybrid procedure
30 is that many eukaryotic transcriptional activators, including those in yeast, consist of two discrete modular domains. The first is a DNA-binding domain that binds to a specific promoter sequence and the second is an activation domain that directs the RNA polymerase II complex to
35 transcribe the gene downstream of the DNA binding site. Both domains are required for transcriptional activation as neither domain can activate transcription on its own.

In the yeast two-hybrid procedure, the gene of interest or parts thereof (BAIT), is cloned in such a way that it is expressed as a fusion to a peptide that has a DNA binding domain. A second gene, or number of genes, such as those from a cDNA library (TARGET), is cloned so that it is expressed as a fusion to an activation domain. Interaction of the protein of interest with its binding partner brings the DNA-binding peptide together with the activation domain and initiates transcription of the reporter genes.

5 The first reporter gene will select for yeast cells that contain interacting proteins (this reporter is usually a nutritional gene required for growth on selective media). The second reporter is used for confirmation and while being expressed in response to interacting proteins it is

10

15

usually not required for growth.

KCNQ2 interactors

Despite the identification of a number of KCNQ2 mutations responsible for epilepsy, including those of the present study, the underlying biological mechanisms responsible for the epilepsy remains largely uncharacterized. Towards identifying these mechanisms, the large intracellular C-terminal region of KCNQ2 was screened for interactions with other proteins using the yeast-two hybrid procedure. The C-terminus accounts for 63% of the KCNQ2 protein and, in common with other KCNQ subunits, contains a conserved 'A domain' (Jentsch, 2000; Schwake et al., 2000) thought to be involved in subunit interactions as well as another distal short conserved region that has been associated with subunit assembly, at least in KCNQ1 (Jentsch, 2000; Schmitt et al., 2000).

A) Yeast-two hybrid analysis

A yeast two-hybrid screen was carried out using the ProQuest™ Two-Hybrid System with Gateway™ Technology (Invitrogen™) according to manufacturer's directions. A KCNQ2 C-terminal entry (BAIT) clone was generated using

the pENTR Directional TOPO® Cloning Kit (Invitrogen™). The following primers were designed to amplify the intracellular C-terminal region of KCNQ2 based on the sequence of human KCNQ2 (Genbank accession number 5 NM_172107): KCNQ2F: 5'-CACCAAGGTTCAGGAGCACAGG-3' and KCNQ2R: 5'-TCACCTCCTGGGCCCGGCCAGCC-3'. The 1611 base pair cloned fragment included exon 10a (found in all our amplified clones), corresponding to amino acid 373-382 of the KCNQ2 protein. The extra 30 base pairs (10 amino acids) were included in our numbering. The PCR-product was 10 cloned into the pENTR/D-TOPO® vector (Invitrogen™) via the TOPO® Cloning reaction according to the manufacturer's instructions. Following sequence verification, the KCNQ2 cDNA fragment was then subcloned into pDEST™32, the DNA 15 Binding domain (DB) Gateway™ Destination Vector (Invitrogen™).

The ProQuest™ Two-Hybrid human brain cDNA Library (TARGET) with Gateway™ technology (ResGen™, Invitrogen™ Corporation) was amplified according to the manufacturer's 20 instructions. Plasmid DNA was purified from the cell pellet using the HiSpeed Plasmid Maxi Kit (Qiagen) according to the manufacturer's instructions.

Both the DBLeu (empty bait vector) and DB-KCNQ2 wild-type (wt) C-term BAITS were transformed into the yeast 25 strain Mav203 and plated onto minimal selective media lacking leucine. A duplicate was carried out where the empty library TARGET (pAD) vector was co-transformed in addition to each BAIT and plated onto minimal selective media lacking leucine (-leu) and tryptophan (-tryp). Yeast 30 control strains (Invitrogen™) were included on all plates. Control 1, used as a negative control, contained empty plasmids pPC97 and pPC86. Control 2 had pPC97-RB and pPC86-E2F1, which express a relatively weak interaction. Control 3 contained plasmids encoding the *Drosophila* DP 35 (pPC97) and E2F (pPC86) domains that have a moderately strong interaction, and provide a control for plasmid shuffling. Control 4 contained pPC97-Fos and pPC86-Jun

which express a relatively strong interaction, and control 5 had a pCL1 plasmid encoding full-length GAL4p and empty pPC86 and was used as a positive control.

5 The constructs were tested for self-activation of the his and β -gal reporter genes according to InvitrogenTM instructions.

For the yeast-two hybrid screen, competent yeast cells were prepared for each BAIT (DB-KCNQ2 wt C-term construct) to be screened, transformed with 31 μ g of 10 ProQuestTM Two-Hybrid human brain AD (activation domain)-cDNA Library and plated onto minimal selective media lacking leucine (-leu), tryptophan (-tryp) and histidine (-his) and containing 3-aminotriazole (+3AT). Positive colonies from each screen were PCR-amplified and re-introduced into fresh yeast cells containing the BAIT to 15 re-test for two-hybrid interaction phenotypes. Those giving rise to more than one PCR product or that failed to re-test positively were systematically eliminated. Positives that re-tested were sequenced using the ABI 20 PRISM[®] BigDye[™] Terminators v3.0 technology. Once identified, the sequence of the potential interactor was checked to verify it was in the same translational frame as the Gal4p-AD encoding sequence of the prey construct.

Approximately 3 x 10⁶ clones from the ProQuestTM Two- 25 Hybrid human brain cDNA Library were screened for interaction with the DB-Q2C wt bait. Among 1039 positive AD-cDNAs recovered, re-tested and subsequently sequenced all were identified as the CALM2 gene, encoding the ubiquitous, Ca²⁺-binding protein, Calmodulin (CaM).

30 The interaction between the C-terminal region of KCNQ2 and CaM has also been reported by other studies (Wen and Levitan, 2002; Yus-Najera et al., 2002; Gamper and Shapiro, 2003). In mammals, the CaM protein is coded by a multigene family consisting of three bona fide members, 35 CALM1, CALM2 and CALM3. Within the non-coding regions of the CaM transcripts, no striking homology is observed, and codon usage is maximally divergent amongst the three CaM

mRNAs that encode an identical protein. It has been hypothesised that the existence of a multigene family provides a tight and complex level of regulatory control at the level of gene expression (Palfi et al., 2002). CaM genes are differentially expressed in the CNS during development and differential regulation of the CaM genes appears necessary to maintain the temporal and spatial fidelity of the CaM protein levels in all subcellular domains. Besides the fundamental housekeeping functions associated with CaM, it is also involved in specialized neuronal functions, such as the synthesis and release of neurotransmitters, neurite extension, long-term potentiation and axonal transport (Palfi et al., 2002).

15 B) Effect of epilepsy-associated KCNQ2 mutations on the CaM-KCNQ2 interaction

To assess the effect that the C-terminus mutations of the present invention had on CaM binding, two of the identified mutations (R353G and L619R) were introduced 20 into the DB-Q2C construct by mutagenesis and were re-analysed for an interaction with CaM using the yeast two-hybrid procedure.

The following primers were used to incorporate the c1057C→G (R353G) and c1856T→G (L619R) changes into the 25 pDEST™32- KCNQ2 C-terminal bait construct.

R353G F 5'-CGCCACCAACCTCTGGGCACAGACCTGCACTC-3'
R353G R 5'-GAGTGCAGGTCTGTGCCCGAGAGGTTGGTGGCG-3'
L619R F 5'-CTTGTCCATGGAGAAGAACGGGACTTCCTGGTAATATC-3'
30 L619R R 5'-GATATTCAACCAGGAAGTCCCGTTCTTCTCCATGGACAAG-3'

Overlapping PCR products were generated using the TOPO® cloning compatible KCNQ2F primer from the initial cloning and the mutagenesis reverse primers, and the 35 KCNQ2R primer from the initial cloning with the mutagenesis forward primers. Products were gel extracted and purified before a second round of PCR using the

initial KCNQ2 F&R primers. These products were also gel extracted before cloning into the pDEST™32 bait vector via the TOPO® system (as described above). Mutant baits were sequence verified.

5 The interaction between each DB-Q2C mutant and CaM was then tested by the yeast two-hybrid assay and compared to the interaction with DB-Q2 wt. Three different PCR-amplified CaM positive clones from the initial screen were re-introduced by gap-repair²⁰ into the prey vector (pPC86) 10 in the yeast strain expressing either DB-Q2C wt, DB-Q2C mutants or the empty DBLeu vector, used as negative control.

15 CaM interaction with the DB-Q2C wt and mutants was then assessed by expression of the *HIS3* and *LacZ* reporter genes.

20 The Q2C R353G mutant did not interact with CaM, as seen by no growth on *HIS3* selective plate (Figure 4C) and no blue readout in the *LacZ* filter assay (Figure 4D-F). On the other hand, the DB-Q2C L619R mutant was shown to still 25 interact with CaM, as seen by growth on *HIS3* selective plate (Figure 4C) and the blue readout in the *LacZ* filter assay. Interestingly, the DB-Q2C L619R mutant showed an even greater growth level on *HIS3* selective plate than the DB-Q2C wt and also appeared to stain faster and more intensely blue in the *LacZ* filter assay, suggesting a stronger interaction between CaM and this mutant.

30 In order to better quantify β -gal activity, a second assay was carried out using the high sensitivity substrate Chlorophenol Red- β -D-Galactopyranoside (CPRG) in liquid culture. The affinity of the DB-Q2C/AD-CaM interaction was measured in terms of units of β -gal activity, with a zero value indicating no expression of the *LacZ* reporter gene, and hence no interaction.

35 In the CPRG assay, a value of 0.05 units β -gal activity (Figure 5) was significantly different from the empty bait vector replicate ($P<0.01$, Student's *t* test), confirming the interaction of the DB-Q2C wt with CaM.

As observed in the LacZ filter assay, the CPRG assay showed a significant difference in the interaction between the Q2C R353G mutant and CaM as compared to the wt replicate ($P<0.01$, Student's t test, Figure 4).

These results suggest that the R353G mutation alters the structural conformation of the KCNQ2 C-terminal domain such that it is no longer able to bind to CaM and that this single point mutation is sufficient to abolish the interaction. By abolishing CaM binding, the R353G mutation could lead to an impairment of M-current *in vivo* due to decreased opening of the channel.

In contrast, the CPRG assay for the L619R Q2C mutant showed a significantly higher level of β -gal activity units (0.26 units) than the wt replicate ($P<0.001$, Student's t test, Figure 5). This finding indicates that the L619R mutation alters the conformation of the protein in a manner that increases CaM binding affinity for the KCNQ2 C-terminal domain by approximately 5-fold. The increased affinity for CaM may affect the ability of the complex to change conformation normally in response to calcium signalling. Alternatively, the marked increase in binding of CaM to the KCNQ2 L619R mutant channel may be detrimental to the M-channel function via disruption of the normal neuronal inhibitory/excitatory balance, therefore causing the seizures associated with epilepsy, particularly BFNS. CaM is known to be involved in both the excitatory and inhibitory neurotransmission pathways (Ohya and Botstein, 1994) and it has been proposed that the temporal and spatial restrictions on CaM itself could enable the tight control of these opposing reactions (Toutenhoofd and Strehler, 2000). Hence, the KCNQ2 L619R mutation could lead to a disruption of the local CaM pool consequently disturbing the finely balanced excitatory and inhibitory neurotransmission systems.

These results implicate CaM in the pathogenesis of epilepsy and specifically in the BFNS syndrome. Whilst further work will be required to fully elucidate the

involvement of the KCNQ2-CaM interaction in neuronal excitability and its correlation with idiopathic epilepsy, these data suggest that dysfunction of this interaction leads to aberrant neuronal excitability in some BFNS patients.

The calmodulin gene (and other ion channel interacting genes) may therefore be a target for mutation in epilepsy as well as other disorders associated with ion channel dysfunction. A mutation in an ion channel interacting gene when expressed alone, or when expressed in combination with one or more other ion channel mutations or ion channel interacting gene mutations (based on the digenic model), may give rise to the disorder. The nature of the ion channel interacting genes and proteins can be studied such that these partners can also be targets for drug discovery.

Industrial Applicability

The mutant ion channel receptor subunits of the invention are useful in the diagnosis and treatment of diseases such as epilepsy and disorders associated with

5 ion channel dysfunction including, but not limited to, hyper- or hypo-kalemic periodic paralysis, myotonias, malignant hyperthermia, myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's disease, Parkinson's disease, schizophrenia, hyperekplexia,

10 anxiety, depression, phobic obsessive symptoms, neuropathic pain, inflammatory pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease, Dent's disease, hyperinsulinemic hypoglycemia of infancy, cystic fibrosis, congenital stationary night blindness and total

15 colour-blindness.

TABLE 1

Examples of mutations and variations identified in ion channel subunit genes

Subunit Gene	Exon/Intron	DNA Mutation	Amino Acid Change	SEQ ID NOS
Sodium Channel Subunits				
Coding exonic variants - amino acid change				
SCN1B ^c	Exon 3	c254G→A	R85H	1, 63
SCN2A ^c	Exon 6A	c668G→A	R223Q	2, 64
SCN2A ^c	Exon 16	c2674G→A	V892I	3, 65
SCN2A ^c	Exon 17	c3007C→A	L1003I	4, 66
SCN2A ^c	Exon 19	c3598A→G	T1200A	5, 67
SCN2A ^c	Exon 20	c3956G→A	R1319Q	6, 68
Coding exonic variants - no amino acid change				
SCN2A ^c	Exon 12	c1785T→C	-	7
SCN2A ^c	Exon 27	c4919T→A	-	8
Non-coding variants				
SCN1A ^c	Intron 23	IVS23+33G→A	-	9
SCN2A ^c	Intron 7	IVS7+61T→A	-	10
SCN2A ^c	Intron 19	IVS19-55A→G	-	11
SCN2A ^c	Intron 22	IVS22-31A→G	-	12
SCN2A ^c	Intron 2	IVS2-28G→A	-	13
SCN2A ^c	Intron 8	IVS8-3T→C	-	14
SCN2A ^c	Intron 11	IVS11+49A→G	-	15
SCN2A ^c	Intron 11	IVS11-16C→T	-	16
SCN2A ^c	Intron 17	IVS17-71C→T	-	17
SCN2A ^c	Intron 17	IVS17-74delG	-	18
SCN2A ^c	Intron 17	IVS17-74insG	-	19
Nicotinic Acetylcholine Receptor Subunits				
Coding exonic variants - amino acid change				
CHRNA5 ^c	Exon 4	c400G→A	V134I	20, 69
CHRNA2 ^c	Exon 4	c373G→A	A125T	21, 70
CHRNA3 ^c	Exon 2	c110G→A	R37H	22, 71
Coding variants - no amino acid change				
CHRNA2 ^c	Exon 4	c351C→T	-	23
CHRNA2 ^c	Exon 5	c771C→T	-	24
CHRNA3 ^c	Exon 2	c159A→G	-	25
CHRNA3 ^c	Exon 4	c291G→A	-	26
CHRNA3 ^c	Exon 4	c345G→A	-	27
Non-coding variants				
CHRNA2 ^c	Intron 3	IVS3-16C→T	-	28
CHRNA3 ^c	Intron 3	IVS3-5T→C	-	29
CHRNA3 ^c	Intron 4	IVS4+8G→C	-	30

Potassium Channel Subunits

Coding exonic variants - amino acid change				
KCNQ2 ^a	Exon 1	c204-c205insC	K69fsX119	31, 72
KCNQ2 ^a	Exon 1	c1A→G	M1V	32
KCNQ2 ^a	Exon 1	c2T→C	M1T	33
KCNQ2 ^a	Exon 8	c1057C→G	R353G	34, 73
KCNQ2 ^a	Exon 11	c1288C→T	R430X	35, 74
KCNQ2 ^a	Exon 14	c1710A→T	R570S	36, 75
KCNQ2 ^a	Exon 15	c1856T→G	L619R	37, 76
Non-coding variants				
KCNQ2 ^a	Intron 9	IVS9+(46-48)delCCT	-	38
KCNQ3 ^a	Intron 11	IVS11+43G→A	-	39
KCNQ3 ^a	Intron 12	IVS12+29G→A	-	40

GABA Receptor Subunits

Coding exonic variants - no amino acid change				
GABRB1 ^c	Exon 5	c508C→T	-	41
GABRB1 ^c	Exon 9	c1329G→A	-	42
GABRB1 ^c	Exon 8	c975C→T	-	43
GABRG3 ^c	Exon 8	c995T→C	-	44
Non-coding variants				
GABRA1 ^c	5' UTR	c-142A→G	-	45
GABRA1 ^c	5' UTR	c-31C→T	-	46
GABRA2 ^c	3' UTR	c1615G→A	-	47
GABRA5 ^c	5' UTR	c-271G→C	-	48
GABRA5 ^c	5' UTR	c-228A→G	-	49
GABRA5 ^c	5' UTR	c-149G→C	-	50
GABRB2 ^b	5' UTR	c-159C→T	-	51
GABRB2 ^c	3' UTR	c1749C→T	-	52
GABRPi ^c	5' UTR	c-101C→T	-	53
GABRB1 ^c	Intron 1	IVS1+24T→G	-	54
GABRB1 ^c	Intron 5	IVS6+72T→G	-	55
GABRB1 ^c	Intron 7	IVS7-34A→G	-	56
GABRB3 ^c	Intron 1	IVS1-14C→T	-	57
GABRB3 ^c	Intron 7	IVS7+58delAA	-	58
GABRD ^c	Intron 6	IVS6+132insC	-	59
GABRD ^c	Intron 6	IVS6+130insC	-	60
GABRD ^c	Intron 6	IVS6+73del	-	61
		CGCGCCCCACCGCCCCCTTCCGCG		
GABRG3 ^c	Intron 8	IVS8-102C→T	-	62

Note: ^a Mutations or variations only occurring in individuals with epilepsy; ^b Variant seen only in normal control samples; ^c Mutations or variants seen in individuals with epilepsy as well as normal control samples. The KCNQ2 numbering is based on the large isoform (inclusion of exon 10a). The numbering of exons and introns for SCN2A is based on the publication of Kasai et al., 2001.

References

References cited herein are listed on the following pages, and are incorporated herein by this reference.

- 5 Andermann, E. (1982). In: *Genetic basis of the epilepsies*. Anderson, VE. Hauser, WA. Penry, JK. and Singh, CF. (Editors). New York, Raven Press. 355-374.
- 10 Aneggers, JF. (1996). *The treatment of epilepsy: Principles and practice*. Second Edition. (Wyllie E (Ed) Williams and Wilkins).
- Bell, JI. and Lathrop, M. (1996). *Nature Genet.* 13: 377-378.
- Berkovic, SF. Andermann, F. Andermann, E. and Gloor, P. (1987). *Neurology* 37: 993-1000.
- 15 Berkovic, SF. Reutens, DC. Andermann, E. and Andermann, F. (1994). In: *Epileptic seizures and syndromes*. Wolf, P. (Editor). London: John Libbey. 25-37.
- Berkovic, SF. Mazarib, A. Neufeld, M. et al. (2000). *Neurology (Supplement 3)*. 54: A356.
- 20 Biervert, C. Schroeder, BC. Kubisch, C. Berkovic, SF. Propping, P. Jentsch, TJ. and Steinlein, OK. (1998). *Science* 279: 403-406.
- Breaker, RR. and Joyce, GF. (1995). *Chem. Biol.* 2: 655-600.
- 25 Cavazzuti, GB. Capella, L. and Nalin, A. (1980). *Epilepsia* 21: 43-55.
- Charlier, C. Singh, NA. Ryan, SG. Lewis, TB. Reus, BE. Leach, RJ. and Leppert, M. (1998). *Nature Genet.* 18: 53-55.
- 30 Cole, SP. Campling, BG. Atlaw, T. Kozbor, D. and Roder, JC. (1984). *Mol. Cell Biochem.* 62: 109-120.
- Collins, FS. (1995). *Nature Genet.* 9: 347-350.
- Commission on Classification and Terminology of the International League against Epilepsy. (1989). *Epilepsia* 30: 389-399.
- 35

- Cote, RJ. Morrissey, DM. Houghton, AN. Beattie, EJ Jr.
Oettgen, HF. and Old, LJ. (1983). Proc. Natl. Acad.
Sci. USA 80: 2026-2030.
- Doose, H. and Baier, WK. (1987). Neuropediatrics 18
5 (Supplement 1): 1-64.
- Doose, H. and Baier, W. (1989). Clev. Clin. J. Med. 56
(Supplement): s105-s110.
- Dworakowska, B. and Dolowy, K. (2000). Acta Biochim. Pol.
47: 685-703.
- 10 Escayg, A. MacDonald, BT. Meisler, MH. Baulac, S.
Huberfeld, G. An-Gourfinkel, I. Brice, A. LeGuern, E.
Moulard, B. Chaigne, D. Buresi, C. and Malafosse, A.
(2000). Nature Genet. 24: 343-345.
- Fong, GC. Shah, PU. Gee, MN. Serratosa, JM. Castroviejo,
15 IP. Khan, S. Ravat, SH. Mani, J. Huang, Y. Zhao, HZ.
Medina, MT. Treiman, LJ. Pineda, G. and Delgado-
Escueta, AV. (1998). Am. J. Hum. Genet. 63: 1117-1129.
- Gamper, N. and Shapiro, MS. (2003). J. Gen. Physiol. 122:
17-31.
- 20 Gardiner, M. (2000). J Neurol. 247: 327-334.
- Goldman, CK. Soroceanu, L. Smith, N. Gillespie, GY. Shaw,
W. Burgess, S. Bilbao, G. and Curiel, DT. (1997). Nature
Biotechnology 15: 462-466.
- Gonzalez, JE. et al. (1999). Drug Discov. Today 4: 431-
25 439.
- Greenberg, DA. Delgado-Escueta, AV. Maldonado, HM. and
Widelitz, H. (1988a). Genet Epidemiol. 5: 81-94.
- Greenberg, DA. Delgado-Escueta, AV. Widelitz, H. Sparkes,
RS. Treiman, L. Maldonado, HM. Park, MS. and Terasaki,
30 PI. (1988b). Am. J. Med. Genet. 31: 185-192.
- Greenberg, DA. Durner, M. and Delgado-Escueta, AV. (1992).
Neurology 42 (Suppl 5): 56-62.
- Hamill, OP. et al. (1981). Pflugers Arch. 391: 85-100.
- Hasseloff, J. and Gerlach, WL. (1988). Nature 334: 585-591.
- 35 Hauser, WA. Annegers, JF. and Kurland, LT. (1993).
Epilepsia 34: 453-468.

- Heller, RA. Schena, M. Chai, A. Shalon, D. Bedilion, T.
Gilmore, J. Woolley, DE. and Davis RW. (1997). *Proc.*
Natl. Acad. Sci. USA 94: 2150-2155.
- Huse, WD. Sastry, L. Iverson, SA. Kang, AS. Alting-Mees,
5 Burton, DR. Benkovic, SJ. and Lerner, RA. (1989).
Science 246: 1275-1281.
- Italian League Against Epilepsy Genetic Collaborative
Group. (1993). *Epilepsia* 34: 819-26.
- Janz, D. Beck-Mannagetta, G. and Sander, T. (1992).
10 *Neurology* 42 (Suppl 5): 48-55.
- Jentsch, TJ. (2000). *Nature Rev. Neurosci.* 1: 21-29.
- Kasai, N. Fukushima, K. Ueki, Y. Prasad, S. Nosakowski, J.
Sugata, K. Sugata, A. Nishizaki, K. Meyer, NC. and
Smith, RJ. (2001). *Gene* 264: 113-122.
- 15 Kohler, G. and Milstein, C. (1975). *Nature* 256: 495-497.
- Kozbor, D. Abramow-Newerly, W. Tripputi, P. Cole, SP.
Weibel, J. Roder, JC. and Croce, CM. (1985). *J.*
Immunol. Methods 81:31-42.
- Lernmark, A. and Ott, J. (1998). *Nature Genet.* 19: 213-
20 214.
- Ohya, Y. and Botstein, D. (1994). *Science* 263: 963-966.
- Okubo, Y. Matsuura, M. Asai, T. Asai, K. Kato, M. Kojima,
T. and Toru, M. (1994). *Epilepsia* 35: 832-841.
- Orlandi, R. Gussow, DH. Jones, PT. and Winter, G. (1989).
25 *Proc. Natl. Acad. Sci. USA* 86: 3833-3837.
- Palfi, A. Kortvely, E. Fekete, E. Kovacs, B. Varszegi, S.
and Gulya, K. (2002). *Life Sciences* 70: 2829-2855.
- Panayiotopoulos, CP. and Obeid, T. (1989). *Ann. Neurol.*
25: 440-443.
- 30 Phillips, HA. Favre, I. Kirkpatrick, M. Zuberi, SM.
Goudie, D. Heron, SE. Scheffer, IE. Sutherland, GR.
Berkovic, SF. Bertrand, D. and Mulley, JC. (2001). *Am.*
J. Hum. Genet. 68: 225-231.
- Reutens, DC. and Berkovic, SF. (1995). *Neurology* 45: 1469-
35 1476.
- Rickert, RC. Roes, J. and Rajewsky, K. (1997). *Nucleic*
Acids Res. 25: 1317-1318.

- Risch, N. and Botstein, D. (1996). *Nature Genet.* 12: 351-353.
- 5 Roger, J. Bureau, M. Dravet, C. Dreifuss, FE. Perret, A. and Wolf, P. (1992). *Epileptic syndromes in infancy, childhood and adolescence.* 2nd Edition. London, John Libbey.
- Scharf, KD. Materna, T. Treuter, E. and Nover, L. (1994). *Results Probl. Cell Differ.* 20: 125-162.
- Scheffer, IE. and Berkovic, SF. (1997). *Brain* 120: 479-90.
- 10 Schena, M. Shalon, D. Heller, R. Chai, A. Brown, PO. and Davis, RW. (1996). *Proc. Natl. Acad. Sci. USA* 93: 10614-10619.
- Schmitt, N. Schwarz, M. Peretz, A. Abitbol, I. Attali, B. and Pongs, O. (2000). *Embo J.* 19: 332-340.
- 15 Schwake, M. Pusch, M. Kharkovets, T. and Jentsch, TJ. (2000). *J. Biol. Chem.* 275: 13343-13348.
- Schwenk, F. Baron, U. and Rajewsky, K. (1995). *Nucleic Acids Res.* 23: 5080-5081.
- Singh, NA. Charlie, C. Stauffer, D. DuPont, ER. Leach, RJ.
- 20 Melis, R. Ronen, GM. Bjerre, I. Quattlebaum, T. Murphy, JV. McHarg, ML. Gagnon, D. Rosales, TO. Peiffer, A. Anderson, VE. and Leppert, M. (1998). *Nature Genet.* 18: 25-29.
- Singh, R. Scheffer, IE. Crossland, K. and Berkovic, SF.
- 25 (1999). *Ann. Neurol.* 45: 75-81.
- Steinlein, OK. Mulley, JC. Propping, P. Wallace, RH. Phillips, RA. Sutherland, GR. Scheffer, IE. and Berkovic, SF. (1995). *Nature Genet.* 11: 201-203.
- Todd, JA. (1999). *Lancet* 354 (Supplement 1): 15-16.
- 30 Toutenhoofd, SL. and Strehler, EE. (2000). *Cell Calcium* 28: 83-96.
- Wallace, RH. Marini, C. Petrou, S. Harkin, LA. Bowser, DN. Panchal, RG. Williams, DA. Sutherland, GR. Mulley, JC. Scheffer, IE. and Berkovic, SF. (2001a). *Nature Genet.*
- 35 28: 49-52.
- Wallace, RH. Scheffer, IE. Barnett, S. Richards, M. Dibbens, L. Desai, RR. Lerman-Sagie, T. Lev, D.

- Mazarib, A. Brand, N. Ben-Zeev, B. Goikhman, I. Singh,
R. Kremmidiotis, G. Gardner, A. Sutherland, GR.
George, AL Jr. Mulley, JC. and Berkovic, SF. (2001b).
Am. J. Hum. Genet. 68: 859-865.
- 5 Wallace, RH. Wang, DW. Singh, R. Scheffer, I. George, A.
Phillips, H. Saar, K. Reis, A. Johnson, E. Sutherland,
G. Berkovic, S. and Mulley, J. (1998). *Nature Genet.*
19: 366-370.
- Wen, H. and Levitan, IB. (2002). *J. Neurosci.* 22: 7991-
10 8001.
- Winter, G. and Milstein, C. (1991). *Nature* 349: 293-299.
- Wyman, AR. and White, R. (1980). *Proc. Natl. Acad. Sci.*
77: 6754-6758.
- Yus-Najera, E. Santana-Castro, I. and Villarroel, A.
15 (2002). *J. Biol. Chem.* 277: 28545-28553.
- Zara, F. Bianchi, A. Avanzini, G. Di Donato, S.
Castellotti, B. Patel, PI. and Pandolfo, M. (1995).
Hum. Mol. Genet. 4: 1201-1207.
- Zara, F. Gennaro, E. Stabile, M. Carbone, I. Malacarne, M.
20 Majello, L. Santangelo, R. de Falco, FA. and
Bricarelli, FD. (2000). *Am. J. Hum. Genet.* 66: 1552-
1557.
- 25 Dated this 7th day of August 2003
- BIONOMICS LIMITED
- By their Patent Attorneys
- GRIFFITH HACK
- Fellows Institute of Patent and
- 30 Trade Mark Attorneys of Australia

Abstract

A method of identifying a subject predisposed to a disorder associated with ion channel dysfunction, comprising ascertaining whether at least one of the genes 5 encoding ion channel subunits in said subject has undergone a mutation event as set forth in one of SEQ ID Numbers: 1-62.

Figure 1

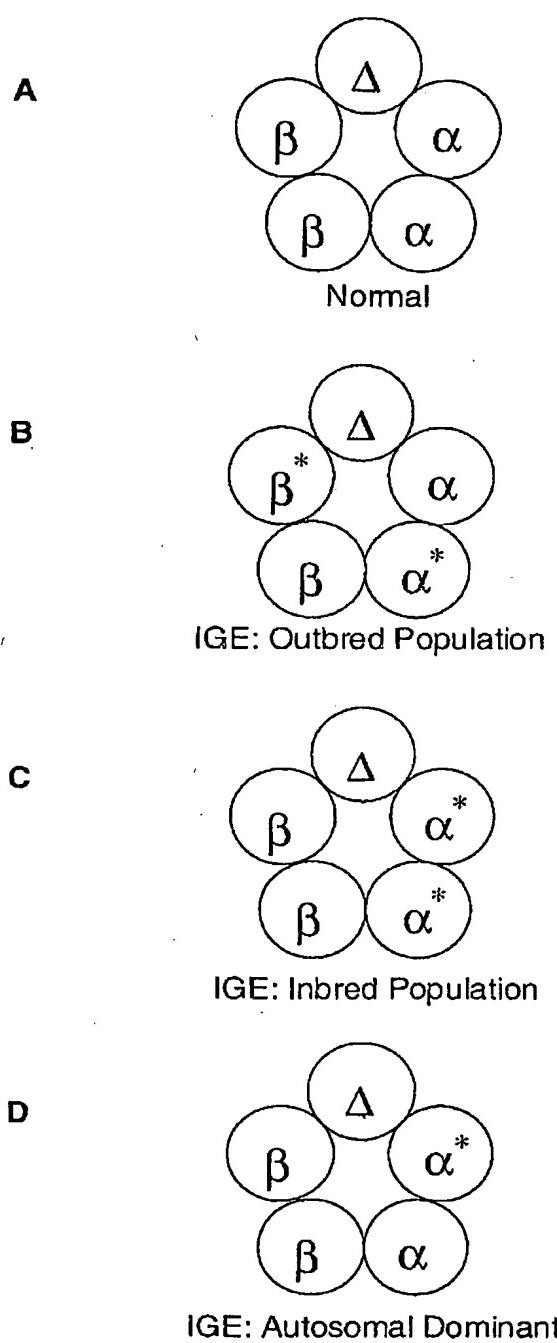


Figure 2

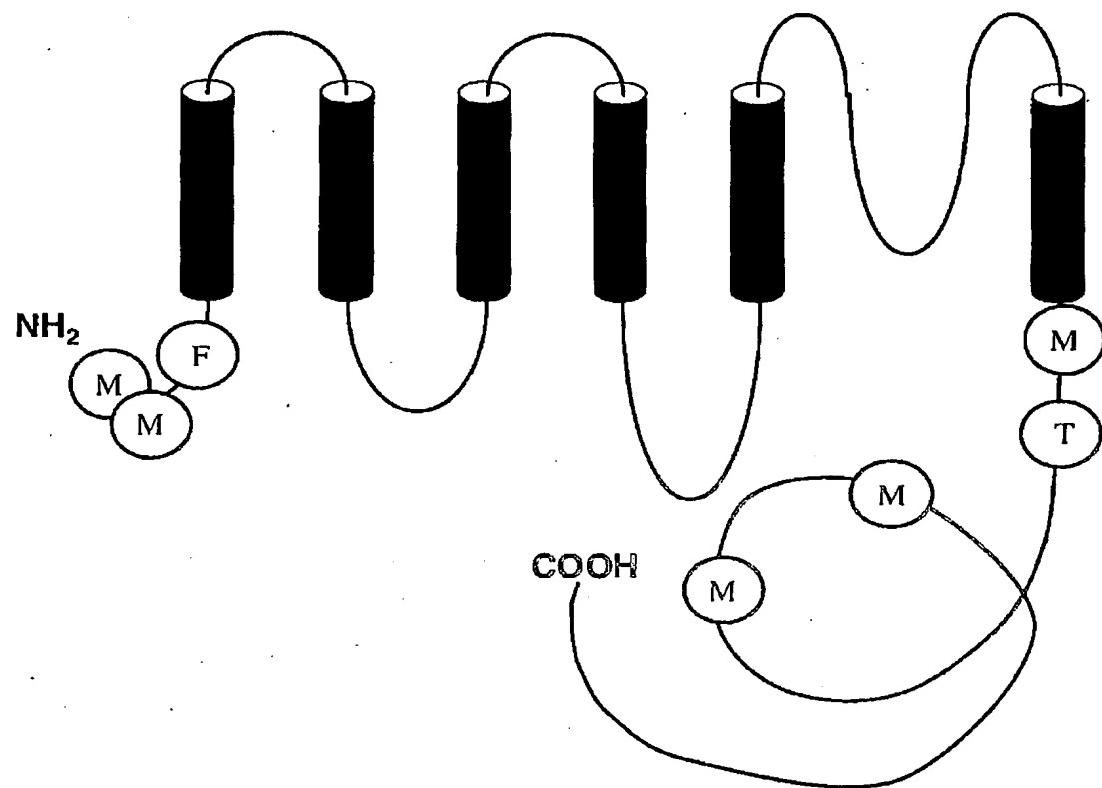
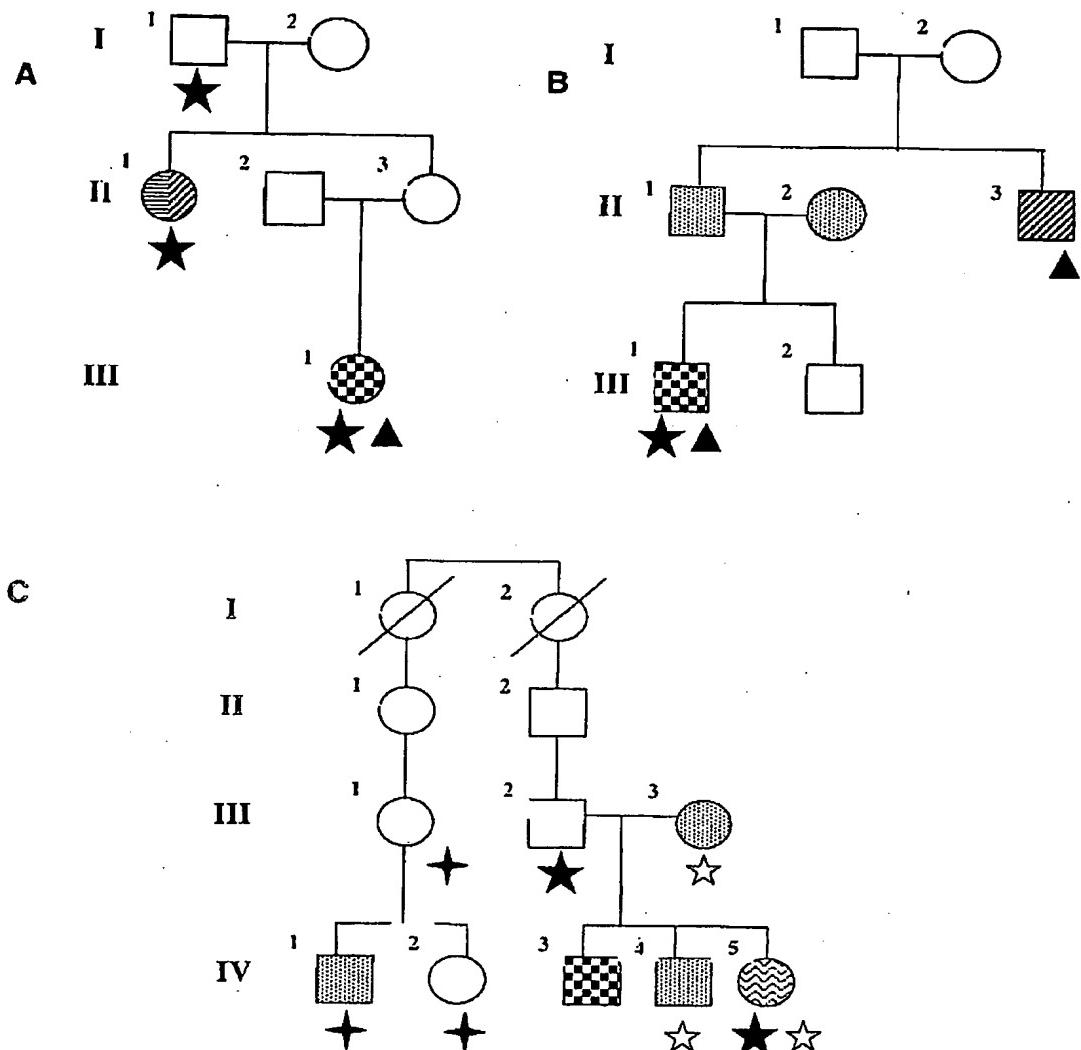


Figure 3



[diagonal lines] Febrile Seizures

[checkered] Febrile Seizures Plus

[wavy lines] Myoclonic Astatic Epilepsy

[horizontal lines] Absences

[vertical lines] Severe Myoclonic Epilepsy of Infancy

▲ A1067T SCN1A

★ N43del SCN3A

† G1050S SCN8A

☆ Q351X GABRG2

Figure 4

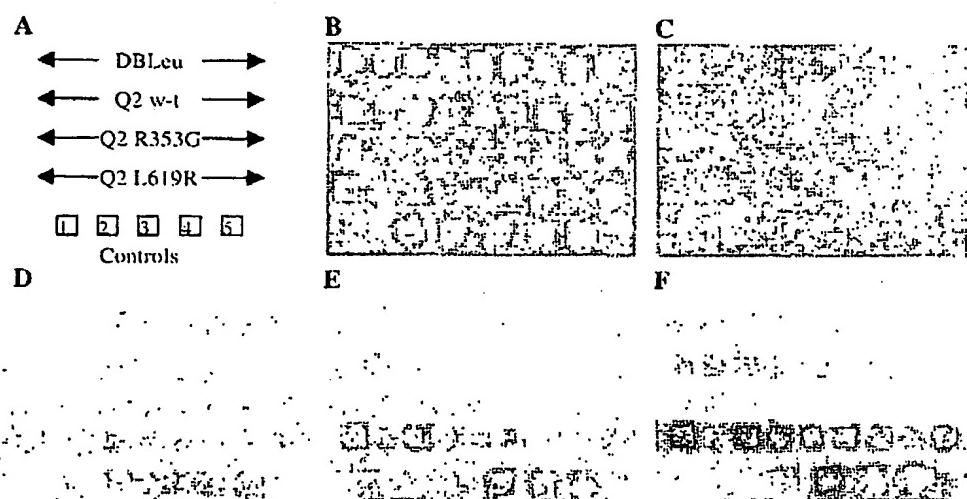
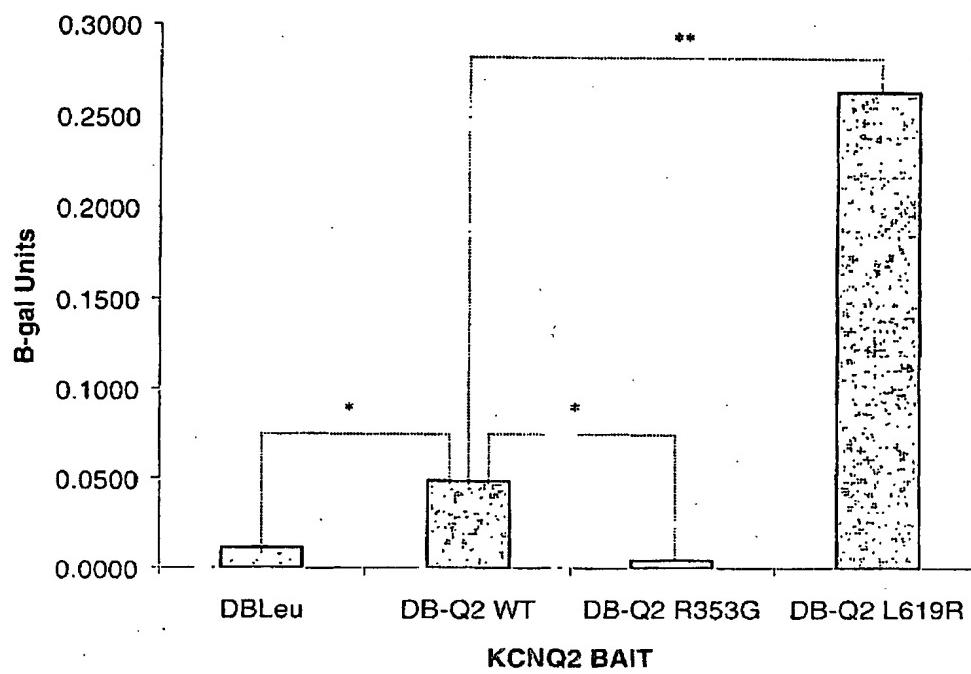


Figure 5



SequencesSSCPRe-file7August03.ST25.txt
SEQUENCE LISTING

<110> Bionomics Limited

<120> P10

<130> SSCP Prov Update 2003

<160> 76

<170> PatentIn version 3.2

<210> 1

<211> 1414

<212> DNA

<213> Homo sapiens

<400> 1

gctccggggg acattctaac cgccgccagg tcccgccgcc tctcgccccg ctattaatac
60

cggcgccccg ggaggggggc gcagcacgag cgcgcagcc atggggaggc tgctggcctt
120

agtggtcggc gcggcaactgg tgtcctcagc ctgcgggggc tgcgtggagg tggactcgga
180

gaccgaggcc gtgtatggga tgaccttcaa aattctttgc atctcctgca agcgccgcag
240

cgagaccaac gctgagaccc tcaccgagtg gaccctccgc cagaaggca ctgaggagtt
300

tgtcaagatc ctgcgtatg agaatgaggt gttgcagctg gaggaggatg agcacttcga
360

ggccgcgtg gtgtggatg gcagccgggg caccaaagac ctgcaggatc tgtctatctt
420

catcaccaat gtcacctaca accactcggg cgactacgag tgccacgtct accgcctgct
480

cttcttcgaa aactacgagc acaacaccag cgtcgtaag aagatccaca ttgaggttagt
540

ggacaaagcc aacagagaca tggcatccat cgtgtctgag atcatgatgt atgtgctcat
600

tgtggtgttg accatatggc tcgtggcaga gatgattac tgctacaaga agatcgctgc
660

cggcacggag actgctgcac aggagaatgc ctggaaatac ctggccatca cctctgaaag
720

caaagagaac tgcacggcgc tccaggtggc cgaatagccc tggccctggg ccccgctca

780

SequencesSSCPRe-file7August03.ST25.txt

aggaagagcc agccgtaatg gggactctcc aggacccgcc tgcccccagc gtgggggtgg
840

ccactcctgg gccccagaaa gcctcagagt cctgccgacg gagccactgg ggtgggaggg
900

ggcagggggc ttggctcgca cccccacttt cgcctcctcc agtcctgccc ccgcggccg
960

cgcacccgcca tgcatgatgg gtaaagcaat actgccgctg cccccaccct gcttctgctg
1020

cctgtttggg gaggggggcg gtgagggtggg ggcagcggcc ccgcacccct cctccttgct
1080

gattgcaca cattggccgc ttcagacacg cacttctggg gccagccct ccccgctcc
1140

tccctgcctg gcggcagggg tcgcgtatgat gggctggagc agtttgggc agggggttct
1200

gggacccact ccgactcccc ctcccccggca tcatttcccc tcccgcttcc tccggctgga
1260

cctgggtcc cccctccctg taatgcactc ctgccccggc ccaacctcgc cctctctcac
1320

cagccttgaa ctgtggccac ctagaaaggg gcccattcag cctcgctct ttacagaagt
1380

agttttgttc atgaaataaa gactttgga cttg
1414

<210> 2

<211> 6328

<212> DNA

<213> Homo sapiens

<400> 2

ttcttggtgc cagcttatca atcccaaact ctgggtgtaa aagattctac agggcacttt
60

cttatgcaag gagctaaaca gtgattaaag gagcaggatg aaaagatggc acagtcagtg
120

ctggtaccgc caggacctga cagcttccgc ttctttacca ggaaatccct tgctgctatt
180

gaacaacgcga ttgcagaaga gaaagctaag agacccaaac aggaacgc当地 ggatgaggat
240

gatgaaaatg gccc当地 aaacagtgc当地 ttggaaagc当地 gaaaatctct tccattt当地

SequencesSSCPRe-file7August03.ST25.txt

300

tatggagaca ttcctccaga gatgggtca gtgcctcgg aggatctgga cccctactat
360

atccaataaga aaacgtttat agtattgaat aaaggaaag caatctctcg attcagtgc
420

accctgccc tttacatccc aactcccttc aaccctatta gaaaatttagc tattaagatt
480

ttggtagatt ctttattcaa tatgctcatt atgtgcacga ttcttaccaa ctgtgtatcc
540

atgaccatga gtaaccctcc agactggaca aagaatgtgg agtatacctt tacaggaatt
600

tatacttttg aatcacttat taaaatactt gcaagggct tttgtttaga agatttcaca
660

tttttacggg atccatggaa ttgggtggat ttcacagtca ttactttgc atatgtgaca
720

gagtttgtgg acctggcaa tgtctcagcg ttgagaacat tcagagttct ccaagcattg
780

aaaacaattt cagtcattcc aggctgaag accattgtgg gggccctgat ccagtcagtg
840

aagaagcttt ctgatgtcat gatcttgcact gtgttctgca taagcgtgtt tgctctaata
900

ggattgcagt tgttcatggg caacctacga aataaatgtt tgcaatggcc tccagataat
960

tcttcctttg aaataaatat cacttccttc tttaacaatt cattggatgg gaatggtaact
1020

actttcaata ggacagttag catatttaac tggatgaat atattgagga taaaagtcac
1080

ttttatcccc tagagggca aatgatgct ctgccttgc gcaacagctc agatgcaggc
1140

cagtgcctg aaggatacat ctgtgtgaag gctggtagaa accccaacta tggctacacg
1200

agcttgaca ccttagttg ggccttttg tccttatttc gtctcatgac tcaagacttc
1260

tggaaaaacc tttatcaact gacactacgt gctgctggaa aaacgtacat gatatcccc
1320

gtgctggta ttttcttggg ctcattctat ctaataaaatt tgatcttgc tgggtggcc
1380

SequencesSSCPre-file7August03.ST25.txt

atggcctatg aggaacagaa tcaggccaca ttgaaagagg ctgaacagaa ggaagctgaa
1440

tttcagcaga tgctcgaaaa gttaaaaaag caacaagaag aagctcaggc ggcagctgca
1500

gccgcattcg ctgaatcaag agacttcagt ggtgctggtg ggataggagt ttttcagag
1560

agttcttcag tagcatctaa gttgagctcc aaaagtgaaa aagagctgaa aaacagaaga
1620

aagaaaaaaga aacagaaaaga acagtctgga gaagaagaga aaaatgacag agtcctaaaa
1680

tcggaatctg aagacagcat aagaagaaaa ggttccgtt ttcccttggaa aggaagttagg
1740

ctgacatatg aaaagagatt ttcttctcca caccagtcct tactgagcat ccgtggctcc
1800

ctttctctc caagacgcaa cagtagggcg agcctttca gttcagagg tcgagcaaag
1860

gacattggct ctgagaatga ctttgctgat gatgagcaca gcacctttga ggacaatgac
1920

agccgaagag actctctgtt cgtccgcac agacatggag aacggcgcca cagcaatgtc
1980

agccaggcca gccgtgcctc cagggtgctc cccatcctgc ccatgaatgg gaagatgcat
2040

agcgctgtgg actgcaatgg tgggtctcc ctggcgcccc gccccttctac cctcacatct
2100

gctggcagc tcctaccaga gggcacaact actgaaacag aaataagaaa gagacggtcc
2160

agttcttatac atgtttccat ggatttattt gaagatccta catcaaggca aagagcaatg
2220

agtatagcca gtatggac caacaccatg gaagaacttg aagaatccag acagaaatgc
2280

ccaccatgct ggtataaatt tgctaataatg tgggtgattt gggactgttg taaaccatgg
2340

ttaaaggta aacacccgtt caacctggtt gtaatggacc catttggatc cctggccatc
2400

accatctgca ttgtcttaaa tacactcttc atggctatgg agcactatcc catgacggag
2460

SequencesSSCPRe-file7August03.ST25.txt

cagttcagca gtgtactgtc tttggaaac ctggcttca caggatctt cacagcagaa
2520

atgtttctca agataattgc catggatcca tattattact ttcaagaagg ctgaaatatt
2580

tttgatggtt ttattgttag ccttagttta atggaaacttg gtttggcaaa tgtggaaagga
2640

ttgtcagttc tccgatcatt ccggctgctc cgagtttca agttggcaaa atcttggcca
2700

actctaaata tgctaattaa gatcattggc aattctgtgg gggctctagg aaacctcacc
2760

ttggtattgg ccatcatcg ttcattttt gctgtggtcg gcatgcagct ctggtaag
2820

agctacaaag aatgtgtctg caagatttc aatgattgtg aactcccacg ctggcacatg
2880

catgactttt tccactcctt cctgatcg ttcogcgtgc tgtgtggaga gtggatagag
2940

accatgtggg actgtatgga ggtcgctggc caaaccatgt gccttactgt ctcatgatg
3000

gtcatggtga ttggaaatct agtggttctg aacctcttct tggccttgct ttgagttcc
3060

ttagttctg acaatctgc tgccactgat gatgataacg aaatgaataa tctccagatt
3120

gctgtggaa ggatgcagaa aggaatcgat ttgttaaaa gaaaaatacg tgaatttatt
3180

cagaaagcct ttgttagaa gcagaaagct ttagatgaaa ttaaaccgct tgaagatcta
3240

aataataaaa aagacagctg tatttccaac cataccacca tagaaatagg caaagacctc
3300

aattatctca aagacggaaa tggaaactact agtggcatag gcagcagtgt agaaaaatata
3360

gtcgtggatg aaagtgatta catgtcattt ataaacaacc ctgcctcac tgtgacagta
3420

ccaattgctg ttggagaatc tgactttgaa aatttaata ctgaagaatt cagcagcgg
3480

tcagatatgg aggaaagcaa agagaagcta aatgcaacta gttcatctga aggcagcacg
3540

gttgatattg gagctccgc cgagggagaa cagcctgagg ttgaacctga ggaatccctt

SequencesSSCPRe-file7August03.ST25.txt

3600

gaacctgaag cctgtttac agaagactgt gtacggaagt tcaagtgttgcagataagc
3660

atagaagaag gcaaaggaa actctggtgg aatttgagga aaacatgcta taagatagtg
3720

gagcacaatt ggtcgaaac cttcattgtc ttcatgattc tgctgagcag tggggctctg
3780

gccttgaag atatatacat tgagcagcga aaaaccatta agaccatgtt agaatatgct
3840

gacaagggtt tcacttacat attcattctg gaaatgctgc taaagtgggt tgcatatgg
3900

tttcaagtgt attttaccaa tgcctggtgc tggctagact tcctgattgt tgatgtctca
3960

ctggtagct taactgcaaa tgcctgggt tactcagaac ttgggccat caaatccctc
4020

agaacactaa gagctctgag gccactgaga gcttgccttgggg aatgagggtt
4080

gttgtaaatg ctcttttagg agccattcca tctatcatga atgtacttct gttttgtctg
4140

atctttggc taatattcag tatcatggga gtgaatctct ttgctggcaa gttttaccat
4200

tgtattaatt acaccactgg agagatgtt gatgtaagcg tggtaacaa ctacagttag
4260

tgccaaagctc tcattgagag caatcaaact gccaggtggaa aaaatgtgaa agtaaaacttt
4320

gataacgtag gacttggata tctgtctcta cttaaagtag ccacgtttaa gggatggatg
4380

gatattatgt atgcagctgt tgattcacga aatgtagaat tacaacccaa gtatgaagac
4440

aacctgtaca tgtatctta tttgtcattc tttattattt ttggttcatt cttaaccttg
4500

aatctttca ttgggtgtcat catagataac ttcaaccaac agaaaaagaa gtttggaggt
4560

caagacattt ttatgacaga agaacagaag aaatactaca atgcaatgaa aaaactgggt
4620

tcaaagaaaac cacaaaaacc catacctcga cctgctaaca aattccaagg aatggtcttt
4680

SequencesSSCPRe-file7August03.ST25.txt

gattttgtaa ccaaacaagt ctttgatatac agcatcatga tcctcatctg ccttaacatg
4740
gtcaccatga tggtgaaac cgatgaccag agtcaagaaa tgacaaacat tctgtactgg
4800
attaatctgg tgttattgt tctgttcact ggagaatgtg tgctgaaact gatctcttt
4860
cgttactact atttcactat tggatggaat attttgatt ttgtggtgtt cattctctcc
4920
attgttagaa tgtttctggc tgaactgata gaaaagtatt ttgtgtcccc taccctgttc
4980
cgagtgatcc gtcttgccag gattggccga atcctacgtc tgatcaaagg agcaaagggg
5040
atccgcacgc tgctcttgc tttgatgatg tcccttcctg cgttgtttaa catcgccctc
5100
cttcctttcc tggcatgtt catctacgcc atcttggga tgtccaattt tgcctatgtt
5160
aagagggaaag ttgggatcga tgacatgttc aactttgaga cctttggcaa cagcatgatc
5220
tgccctgttcc aaattacaac ctctgctggc tggatggat tgctagcacc tattcttaat
5280
agtggaccc tcagactgtga ccctgacaaa gatcacccctg gaagctcagt taaggagac
5340
tgtgggaacc catctgttgg gatttcttt tttgtcagtt acatcatcat atccttcctg
5400
gttgtgctga acatgtacat cgcggtcatac ctggagaact tcagtgttgc tactgaagaa
5460
agtgcagagc ctctgagtga ggatgacttt gagatgttct atgaggtttg ggagaagttt
5520
gatcccgtg cgacccagtt tatagagttt gccaaacttt ctgattttgc agatgccctg
5580
gatcccttc ttctcatagc aaaacccaac aaagtccagc tcattgccat ggatctgccc
5640
atggtgagtg gtgaccggat ccactgtctt gacatcttat ttgcattttac aaagcgtgtt
5700
ttgggtgaga gtggagagat ggatgccctt cgaatacaga tggaagagcg attcatggca
5760

SequencesSSCPRe-file7August03.ST25.txt
tcaaaccctt ccaaagtctc ttatgagccc attacgacca cgttgaaacg caaacaagag
5820

gaggtgtctg ctattattat ccagaggct tacagacgct acctcttcaa gcaaaaagtt
5880

aaaaaggtat caagtatata caagaaagac aaaggcaaag aatgtgatgg aacacccatc
5940

aaagaagata ctctcattga taaactgaat gagaattcaa ctccagagaa aaccgatatg
6000

acgccttcca ccacgtctcc accctcgat gatagtgtga ccaaaccaga aaaagaaaaa
6060

tttggaaaaag acaaattcaga aaaggaagac aaaggaaag atatcagggaa aagtaaaaag
6120

taaaaagaaa ccaagaattt tccattttgt gatcaattgt ttacagcccc tgatggtgat
6180

gtgttgtgt caacaggact cccacaggag gtctatgcc aactgactgt tttacaaat
6240

gtatacttaa ggtcagtgcc tataacaaga cagagaccc tcggtcagcaa actggactc
6300

agtaaactgg agaaatagta tcgatggg
6328

<210> 3
<211> 6328
<212> DNA
<213> Homo sapiens

<400> 3
ttcttggtgc cagcttatca atcccaaact ctgggtgtaa aagattctac agggcacttt
60

cttatgcaag gagctaaaca gtgattaaag gagcaggatg aaaagatggc acagtcagtg
120

ctggtaaccgc caggacctga cagcttccgc ttctttacca ggaaatccct tgctgctatt
180

gaacaacgca ttgcagaaga gaaagctaag agacccaaac aggaacgcaa ggatgaggat
240

gatgaaaatg gcccaaagcc aaacagtgcac ttggaaagcag gaaaatctct tccatttatt
300

tatggagaca ttccatccaga gatgggtgtca gtgcccctgg aggatctgga cccctactat
360

SequencesSSCPRe-file7August03.ST25.txt
atcaataaga aaacgttat agtattgaat aaaggaaag caatctctcg attcagtgcc
420
accctgccc tttacatTTT aactccCTTC aaccctatta gaaaatttagc tattaagatt
480
ttggcacATT ctTTATTCAA tatgctcatt atgtgcacga ttcttaccaa ctgtgtattt
540
atgaccatga gtaaccCTCC agactggaca aagaatgtgg agtatacctt tacaggaatt
600
tatactttg aatcacttat taaaatactt gcaagggct tttgtttaga agatttcaca
660
ttttacggg atccatggaa ttgggtggat ttcacagtca ttactttgc atatgtaca
720
gagtttgtgg acctgggcaa tgtctcagcg ttgagaacat tcagagttct ccgagcattg
780
aaaacaattt cagtcattcc aggCCTGAAG accattgtgg gggccctgat ccagtcagtg
840
aagaagctt ctgatgtcat gatcttGACT gtgttctgtc taagcgtgtt tgcgctaata
900
ggattgcagt tgTCATGGG caacctacga aataaatgtt tgcaatggcc tccagataat
960
tcttcTTTG aaataaatat cacttcTTTC tttaacaatt cattggatgg gaatggtaact
1020
actttcaata ggacagttag catatttaac tggatgaat atattgagga taaaagtac
1080
ttttatTTT tagagggca aaatgtatgt ctgctttgtg gcaacagctc agatgcaggc
1140
cagtgtcctg aaggatacat ctgtgtgaag gctggtagaa accccaacta tggctacacg
1200
agcttgcaca CCTTAGTTG ggcTTTTG tcTTTATTTC gtctcatgac tcaagacttc
1260
tggaaaaacc ttatcaact gacactacgt gctgctggga aaacgtacat gatTTTTT
1320
gtgctggta tttcttggg ctcattctat ctaataaatt tgatcttggc tgggtggcc
1380
atggcctatg aggaacagaa tcaggccaca ttggaagagg ctgaacagaa ggaagctgaa
1440
ttcagcaga tgctcgaaca gttgaaaaag caacaagaag aagctcagggc ggcagctgca

1500

SequencesSSCPRe-file7August03.ST25.txt

gccgcatctg ctgaatcaag agacttcagt ggtgctggtg ggataggagt ttttcagag
1560
agttcttcag tagcatctaa gttgagctcc aaaagtgaaa aagagctgaa aaacagaaga
1620
aagaaaaaaga aacagaaaaga acagtctgga gaagaagaga aaaatgacag agtcctaaaa
1680
tcggaatctg aagacagcat aagaagaaaa ggttccgtt tttccttggaa aggaagtagg
1740
ctgacatatg aaaagagatt ttcttctcca caccagtcc tactgagcat ccgtggctcc
1800
ctttctctc caagacgcaa cagtagggcg agcctttca gcttcagagg tcgagcaaag
1860
gacattggct ctgagaatga ctttgctgat gatgaggcaca gcaccttga ggacaatgac
1920
agccgaagag actctctgtt cgtgccgcac agacatggag aacggcgcca cagcaatgtc
1980
agccaggcca gccgtgcctc cagggtgctc cccatcctgc ccatgaatgg gaagatgcat
2040
agcgctgtgg actgcaatgg tgtggctcc ctggcgaaaa gccccttac cctcacatct
2100
gctggcagc tcctaccaga gggcacaact actgaaacag aaataagaaa gagacggtcc
2160
agttcttatac atgtttccat ggatttattt gaagatccta catcaaggca aagagcaatg
2220
agtatagcca gtatttgac caacaccatg gaagaacttg aagaatccag acagaaatgc
2280
ccaccatgct ggtataaatt tgctaataatg tgtttgattt gggactgttg taaaccatgg
2340
ttaaagggtga aacacccgtt caacctgggt gtaatggacc catttgtga cctggccatc
2400
accatctgca ttgtcttaaa tacactcttc atggctatgg agcactatcc catgacggag
2460
cagttcagca gtgtactgtc tgttggaaac ctggcttca cagggatctt cacagcagaa
2520
atgtttctca agataattgc catggatcca tattattact ttcaagaagg ctggaatatt
2580

SequencesSSCPRe-file7August03.ST25.txt

tttgatggtt ttattgtgag ccttagttt atgaaacttg gtttggcaaa tgtggaagga
2640

ttgtcagttc tccgatcatt ccggctgctc cgagtttca agttggcaaa atcttggcca
2700

actctaaata tgctaattaa gatcattggc aattctgtgg gggctctagg aaacctcacc
2760

tttgtattgg ccatcatcat cttcatttt gctgtggtcg gcatgcagct ctttgttaag
2820

agctacaaag aatgtgtctg caagatttcc aatgattgtg aactcccacg ctggcacatg
2880

catgactttt tccactcctt cctgatcgta ttccgcgtgc tgtgtggaga gtggatagag
2940

accatgtggg actgtatgga ggtcgctggc caaaccatgt gccttactgt cttcatgatg
3000

gtcatggta ttggaaatct agtggttctg aacctctct tggccttgct tttgagttcc
3060

ttagttctg acaatcttgc tgccactgat gatgataacg aaatgaataa tctccagatt
3120

gctgtggaa ggatgcagaa aggaatcgat tttgtaaaaaaa gaaaaatacg tgaatttatt
3180

cagaaagcct ttgttaggaa gcagaaagct ttagatgaaa ttaaaccgct tgaagatcta
3240

aataataaaa aagacagctg tatttccaac cataccacca tagaaatagg caaagacctc
3300

aattatctca aagacggaaa tggaaactact agtggcatag gcagcagtgt agaaaaatata
3360

gtcgtggatg aaagtgatta catgtcattt ataaacaacc ctgcctcac tgtgacagta
3420

ccaattgctg ttggagaatc tgactttgaa aatttaaata ctgaagaatt cagcagcgag
3480

tcagatatgg aggaaagcaa agagaagcta aatgcaacta gttcatctga aggcagcacg
3540

gttgatattg gagctccgcg cggggagaa cagcctgagg ttgaacctga ggaatccctt
3600

gaacctgaag cctgtttac agaagactgt gtacggaagt tcaagtgttgc tcagataagc
3660

SequencesSSCPre-file7August03.ST25.txt

atagaagaag gcaaaggaa actctggtgg aatttgagga aaacatgcta taagatagtg
3720

gagcacaatt ggtcgaaac cttcattgtc ttcatgattc tgctgagcag tggggctctg
3780

gccttgaag atatatacat tgagcagcga aaaaccatta agaccatgtt agaatatgct
3840

gacaagggtt tcacttacat attcattctg gaaatgctgc taaagtgggt tgcataatgg
3900

tttcaagtgt atttaccaa tgcctggtgc tggctagact tcctgattgt tgatgtctca
3960

ctggtagct taactgcaaa tgcctgggt tactcagaac ttgggccat caaatccctc
4020

agaacactaa gagctgttag gccactgaga gctttgtccc ggtttgaagg aatgagggtt
4080

gttgtaaatg ctcttttagg agccattcca tctatcatga atgtacttct gttttgtctg
4140

atctttggc taatattcag tatcatggga gtgaatctct ttgctggcaa gttttaccat
4200

tgtattaatt acaccactgg agagatgtt gatgtaagcg tggtaaccaa ctacagttag
4260

tgcaaagctc tcattgagag caatcaaact gccaggtggaa aaaatgtgaa agtaaacttt
4320

gataacgtag gacttggata tctgtctcta cttcaagtag ccacgtttaa gggatggatg
4380

gatattatgt atgcagctgt tgattcacga aatgtagaat tacaacccaa gtatgaagac
4440

aacctgtaca tgtatctta tttgtcatc tttattattt ttggttcatt ctttaccttg
4500

aatctttca ttgggtcat catagataac ttcaaccaac agaaaaagaa gtttggaggt
4560

caagacattt ttatgacaga agaacagaag aaatactaca atgcaatgaa aaaactgggt
4620

tcaaagaaac cacaaaaacc catacctcga cctgctaaca aattccaagg aatggtcttt
4680

gattttgtaa ccaaacaagt ctttgatatc agcatcatga tcctcatctg ctttaacatg
4740

gtcaccatga tggtgaaac cgatgaccag agtcaagaaa tgacaaacat tctgtactgg

SequencesSSCPRe-file7August03.ST25.txt

4800

attaatctgg tgtttattgt tctgttcact ggagaatgtg tgctgaaact gatctcttt
4860

cgttactact atttcaactat tggatggaaat attttgatt ttgtgggtt cattctctcc
4920

attgttaggaa tgtttctggc tgaactgata gaaaagtatt ttgtgtcccc taccctgttc
4980

cgagtgatcc gtcttgccag gattggccga atcctacgta tcatcaaagg agcaaagggg
5040

atccgcacgc tgctcttgc tttgatgatg tccttcctg cgttgttaa catggcctc
5100

cttctttcc tggtcatgtt catctacgcc atcttgaaa tgtccaattt tgccatgtt
5160

aagagggaaat ttgggatcga tgacatgttc aactttgaga cctttggcaa cagcatgatc
5220

tgcctgttcc aaattacaac ctctgctggc tggatggat tgctagcacc tattcttaat
5280

agtggacctc cagactgtga ccctgacaaa gatcacccctg gaagctcagt taaaggagac
5340

tgtggaaacc catctgttgg gatTTTCTTT tttgtcagtt acatcatcat atccttcctg
5400

gttgtgctga acatgtacat cgcggtcatc ctggagaact tcagtgtgc tactgaagaa
5460

agtgcagagc ctctgagtga ggatgacttt gagatgttct atgaggtttggagaagttt
5520

gatcccgtg cgacccagtt tatagagttt gccaaacttt ctgatttgc agatgccctg
5580

gatccctcctc ttctcatagc aaaacccaaac aaagtccagc tcattgccat ggatctgccc
5640

atggtgagtg gtgacccggat ccactgtttt gacatcttat ttgttttac aaagcgtgtt
5700

ttgggtgaga gtggagagat ggatgccctt cgaatacaga tggaaagagcg attcatggca
5760

tcaaaccctt ccaaagtctc ttatgagccc attacgacca cgttgaaacg caaacaagag
5820

gaggtgtctg ctattattat ccagagggct tacagacgct acctcttgaa gaaaaagtt
5880

SequencesSSCPRe-file7August03.ST25.txt

aaaaaggtat caagtatata caagaaagac aaaggcaaag aatgtgatgg aacacccatc
5940

aaagaagata ctctcattga taaactgaat gagaattcaa ctccagagaa aaccgatatg
6000

acgccttcca ccacgtctcc accctcgat gatagtgtga ccaaaccaga aaaagaaaaa
6060

tttggaaaag acaaatcaga aaaggaagac aaaggaaag atatcaggg aagtaaaaag
6120

taaaaagaaa ccaagaattt tccattttgt gatcaattgt ttacagcccc tgatggat
6180

gtgttgtgt caacaggact cccacaggag gtctatgcc aactgactgt ttttacaaat
6240

gtatacttaa ggtcagtgcc tataacaaga cagagacctc tggtcagcaa actggaaactc
6300

agtaaactgg agaaatagta tcgatggg
6328

<210> 4
<211> 6328
<212> DNA
<213> Homo sapiens

<400> 4
ttcttggtgc cagtttatca atcccaaact ctgggtgtaa aagattctac agggcacttt
60

cttatgcaag gagctaaaca gtgattaaag gagcaggatg aaaagatggc acagtcagt
120

ctggtaccgc caggacctga cagttccgc ttctttacca gggaatccct tgctgttatt
180

gaacaacgca ttgcagaaga gaaagctaag agacccaaac aggaacgcaa ggatgaggat
240

gatgaaaatg gcccaaagcc aaacagtgac ttggaagcag gaaaatctct tccattttatt
300

tatggagaca ttcctccaga gatggtgtca gtgccttgg aggatctgga cccctactat
360

atcaataaga aaacgtttat agtattgaat aaaggaaag caatctctcg attcagtgcc
420

accctgccc tttacatttt aactcccttc aaccctatta gaaaatttagc tattaagatt
480

SequencesSSCPRe-file7August03.ST25.txt

tttgtacatt ctttattcaa tatgctcatt atgtcacga ttcttaccaa ctgtgtattt
540
atgaccatga gtaaccctcc agactggaca aagaatgtgg agtataacctt tacaggaatt
600
tatactttg aatcaacttat taaaatactt gcaagggct tttgtttaga agatttcaca
660
tttttacggg atccatggaa ttgggttgat ttcacagtca ttactttgc atatgtgaca
720
gagtttgcgg acctgggcaa tgtctcagcg ttgagaacat tcagagttct ccgagcattg
780
aaaacaattt cagtcattcc aggctgaag accattgtgg gggccctgat ccagtcagtg
840
aagaagcttt ctgatgtcat gatcttgcact gtgttctgtc taagcgtgtt tgctctaata
900
ggattgcagt tgttcatggg caacctacga aataaatgtt tgcaatggcc tccagataat
960
tcttcctttg aaataaaatat cacttccttc tttaacaatt cattggatgg gaatggtaact
1020
actttcaata ggacagttag catatccaac tggatgaat atattgagga taaaagtcac
1080
ttttatTTT tagagggca aaatgatgtct gtgcTTTGT gcaacagctc agatgcaggc
1140
cagtgtcctg aaggatacat ctgtgtgaag gctggtagaa accccaacta tggctacacg
1200
agctttgaca ccttagtttgc ggcTTTTG tccttatttc gtctcatgac tcaagacttc
1260
tggaaaaacc ttatcaact gacactacgt gctgctggaa aaacgtacat gatatTTT
1320
gtgctggta ttttcttggg ctcattctat ctaataaatt tgatcttggc tgggtggcc
1380
atggcctatg aggaacagaa tcaggccaca ttggaagagg ctgaacagaa ggaagctgaa
1440
tttcagcaga tgctcgaaca gttgaaaaag caacaagaag aagctcaggc ggcagctgca
1500
gccgcatttg ctgaatcaag agacttcagt ggtgctggta ggtataggagt ttttcagag
1560

SequencesSSCPRe-file7August03.ST25.txt

agttcttcag tagcatctaa gttgagctcc aaaagtgaaa aagagctgaa aaacagaaga
1620

aagaaaaaga aacagaaaga acagtctgga gaagaagaga aaaatgacag agtcctaaaa
1680

tcggaatctg aagacagcat aagaagaaaa ggttccgtt ttccttgga aggaagtagg
1740

ctgacatatg aaaagagatt ttcttctcca caccaggcct tactgagcat ccgtggctcc
1800

ctttctctc caagacgcaa cagtagggcg agcctttca gttcagagg tcgagcaaag
1860

gacattggct ctgagaatga ct tgctgat gatgagcaca gcaccttga ggacaatgac
1920

agccgaagag actctctgtt cgtgcccac agacatggag aacggcgcca cagcaatgtc
1980

agccaggcca gccgtgcctc cagggtgctc cccatctgc ccatgaatgg gaagatgcat
2040

agcgctgtgg actgcaatgg tgtggctcc ctggcgcccc gccccttac cttcacatct
2100

gctggcagc tcctaccaga gggcacaact actgaaacag aaataagaaa gagacggtcc
2160

agttcttatac atgtttccat ggatttattt gaagatccta catcaaggca aagagcaatg
2220

agtatagcca gtatttgac caacaccatg gaagaacttg aagaatccag acagaaatgc
2280

ccaccatgct ggtataaatt tgtaatatg ttttgattt gggactgttg taaaccatgg
2340

ttaaaggta aacacccgtt caacctgggt gtaatggacc catttggta cctggccatc
2400

accatctgca ttgtctaaa tacactttc atggctatgg agcactatcc catgacggag
2460

cagttcagca gtgtactgtc tttggaaac ctggcttca cagggatctt cacagcagaa
2520

atgtttctca agataattgc catggatcca tattattact ttcaagaagg ctggatatt
2580

tttgatggtt ttattgttag ccttagttt atggacttg gttggcaaa tgtggagga
2640

ttgtcagttc tccgatcatt ccggctgctc cgagtttca agttggcaaa atcttggcca

2700

SequencesSSCPRe-file7August03.ST25.txt

actctaaata tgctaattaa gatcattggc aattctgtgg gggctctagg aaacctcacc
2760

tttgttattgg ccatcatcg ttcattttt gctgtggtcg gcatgcagct ctttgtaag
2820

agctacaaag aatgtgtctg caagattcc aatgattgtg aactcccacg ctggcacatg
2880

catgactttt tccactcctt cctgatcg ttcgcgtgc tgtgtggaga gtggatagag
2940

accatgtggg actgtatgga gtcgcgtgc caaaccatgt gccttactgt cttcatgatg
3000

gtcatggta ttggaaatct agtggttctg aacctttct tggccttgct tttgagttcc
3060

ttagttctg acaatcttgc tgccactgat gatgataacg aaatgaataa tatccagatt
3120

gctgtggaa ggatgcagaa aggaatcgat tttttaaaaaaa gaaaaatacg tgaattttt
3180

cagaaagcct ttgttaggaa gcagaaagct ttagatgaaa ttaaaccgct tgaagatcta
3240

aataataaaa aagacagctg tatttccaac cataccacca tagaaatagg caaagacctc
3300

aatttatctca aagacggaaa tggaaactact agtggcatag gcagcagtgt agaaaaatata
3360

gtcgtggatg aaagtgatta catgtcattt ataaacaacc ctgcctcac tgtgacagta
3420

ccaattgctg ttggagaatc tgactttgaa aatttaaata ctgaagaatt cagcagcgag
3480

tcaagatatgg aggaaagcaa agagaagcta aatgcaacta gttcatctga aggcagcacg
3540

gttgatattg gagctccgc cgagggagaa cagcctgagg ttgaacctga ggaatccctt
3600

gaacctgaag cctgtttac agaagactgt gtacggaagt tcaagtgttg tcagataagc
3660

atagaagaag gcaaaggaa actctgggg aatttgagga aaacatgcta taagatagtg
3720

gagcacaatt ggtcgaaac cttcattgtc ttcattgtc tgctgagcag tggggctctg
3780

SequencesSSCPRe-file7August03.ST25.txt

gccttgaag atatatacat tgagcagcga aaaaccatta agaccatgtt agaatatgct
3840
gacaagggtt tcacttacat attcattctg gaaatgctgc taaagtgggt tgcatatggt
3900
tttcaagtgt atttaccaa tgcctggtgc tggctagact tcctgattgt tgatgtctca
3960
ctggtagct taactgcaaa tgcctgggt tactcagaac ttggtgccat caaatccctc
4020
agaacactaa gagctctgag gccactgaga gcttgcgtccc gggttgaagg aatgagggtt
4080
gttgtaaatg ctcttttagg agccattcca tctatcatga atgtacttct ggtttgtctg
4140
atctttggc taatattcag tatcatggga gtgaatctct ttgctggcaa gtttaccat
4200
tgtattaatt acaccactgg agagatgtt gatgtaagcg tggtaacaaa ctacagttag
4260
tgcaaagctc tcattgagag caatcaaact gccaggtgga aaaatgtgaa agtaaacttt
4320
gataacgtag gacttggata tctgtctcta cttcaagtag ccacgtttaa gggatggatg
4380
gatattatgt atgcagctgt tgattcacga aatgtagaat tacaacccaa gtatgaagac
4440
aacctgtaca tgtatctta tttgtcattc tttattatc ttggttcatt cttaccttg
4500
aatctttca ttgggtcat catagataac ttcaaccaac agaaaaagaa gtttggaggt
4560
caagacattt ttatgacaga agaacagaag aaatactaca atgcaatgaa aaaactgggt
4620
tcaaagaaac cacaaaaacc catacctcga cctgctaaca aattccaagg aatggtctt
4680
gattttgtaa ccaaacaagt ctttgatatac agcatcatga tcctcatctg ccttaacatg
4740
gtcaccatga tggtgaaac cgatgaccag agtcaagaaa tgacaaacat tctgtactgg
4800
attaatctgg tggattgt tctgttcact ggagaatgtg tgctgaaact gatctcttt
4860

SequencesSSCPRe-file7August03.ST25.txt
cgttactact attcaactat tggatggaaat attttgatt ttgtgggtt cattctctcc
4920
attgttaggaa tgtttctggc tgaactgata gaaaagtatt ttgtgtcccc taccctgttc
4980
cgagtgatcc gtcttgccag gattggccga atcctacgtc tgatcaaagg agcaaagggg
5040
atccgcacgc tgctcttgc tttgatgatg tcccttcctg cgttgtttaa catggcctc
5100
cttctttcc tggcatgtt catctacgcc atcttggaa tgtccaattt tgccatgtt
5160
aagagggaaag ttgggatcga tgacatgttc aactttgaga ccttggcaa cagcatgatc
5220
tgctgttcc aaattacaac ctctgctggc tggatggat tgcttagcacc tattcttaat
5280
agtggaccc cagactgtga ccctgacaaa gatcacccctg gaagctcagt taaaggagac
5340
tgtggaaacc catctgttgg gattttcttt tttgtcagtt acatcatcat atccttcctg
5400
gttgtgctga acatgtacat cgcggtcattc ctggagaact tcagtgttgc tactgaagaa
5460
agtgcagagc ctctgagtga ggatgacttt gagatgttct atgaggtttg ggagaagttt
5520
gatcccgtg cgacccagtt tatagagttt gccaaacttt ctgatTTTgc agatgccctg
5580
gatccctc ttcctatagc aaaacccaaac aaagtccagc tcattgccat ggatctgccc
5640
atggtgagtg gtgaccggat ccactgttcc gacatcttat ttgctttac aaagcgtgtt
5700
ttgggtgaga gtggagagat ggatgccctt cgaatacaga tggaaagagcg attcatggca
5760
tcaaaccctt ccaaagtctc ttatgagccc attacgacca cgttgaaacg caaacaagag
5820
gaggtgtctg ctattattat ccagagggct tacagacgct acctttgaa gcaaaaagtt
5880
aaaaaggtat caagtatata caagaaagac aaaggcaaag aatgtgatgg aacacccatc
5940
aaagaagata ctctcattga taaactgaat gagaattcaa ctccagagaa aaccgatatg

6000

SequencesSSCPRe-file7August03.ST25.txt

acgccttcca ccacgtctcc accctcgat gatagtgtga ccaaaccaga aaaagaaaaaa
6060

tttgaaaaag acaaattcaga aaaggaagac aaaggaaaag atatcaggaa aagtaaaaag
6120

taaaaagaaa ccaagaattt tccatTTTGT gatcaattgt ttacagcccc tgatgggtat
6180

gtgtttgtgt caacaggact cccacaggag gtctatgcc aactgactgt ttttacaaat
6240

gtatacttaa ggtcagtgcc tataacaaga cagagacctc tggtcagcaa actggaaactc
6300

agtaaactgg agaaatagta tcgatggg
6328

<210> 5
<211> 6328

<212> DNA

<213> Homo sapiens

<400> 5

ttcttggtgc cagcttatca atcccaaact ctgggtgtaa aagattctac agggcactt
60

cttatgcaag gagctaaaca gtgattaaag gagcaggatg aaaagatggc acagtcagtg
120

ctggtaccgc caggacctga cagctccgc ttctttacca gggaatccct tgctgttatt
180

gaacaacgca ttgcagaaga gaaagctaag agacccaaac aggaacgcaa ggatgaggat
240

gataaaaatg gcccaaagcc aaacagtgac ttggaagcag gaaaatotct tccatttatt
300

tatggagaca ttcctccaga gatggtgtca gtgcctctgg aggatctgga cccctactat
360

atcaataaga aaacgtttat agtattgaat aaaggaaaag caatctctcg attcagtgcc
420

accctgccc tttacattt aactcccttc aaccctatta gaaaatttagc tattaagatt
480

ttggcacatt ctatttacaa tatgctcatt atgtcacga ttcttaccaa ctgtgttattt
540

atgaccatga gtaaccctcc agactggaca aagaatgtgg agtatacctt tacaggaatt

SequencesSSCPre-file7August03.ST25.txt

600 tatacttttg aatcacttat taaaatactt gcaaggggct tttgtttaga agatttcaca
660 ttttacggg atccatggaa ttgggtggat ttcacagtca ttactttgc atatgtgaca
720 gagtttgtgg acctgggcaa tgtctcagcg ttgagaacat tcagagttct ccgagcattg
780 aaaacaattt cagtcattcc aggccctgaag accattgtgg gggccctgat ccagtcagtg
840 aagaagctt ctgatgtcat gatcttgact gtgttctgtc taagcgtgtt tgcgctaata
900 ggattgcagt tttcatggg caacctacga aataaatgtt tgcaatggcc tccagataat
960 tcttcctttg aaataaaat cacttccttc tttaacaatt cattggatgg gaatggtact
1020 acttcaata ggacagttag catatthaac tgggatgaat atattgagga taaaagtcac
1080 ttttattttt tagaggggca aaatgatgct ctgctttgtg gcaacagctc agatgcaggc
1140 cagtgtcctg aaggatacat ctgtgtgaag gctggtagaa accccaacta tggctacacg
1200 agctttgaca ccttagttg ggccttttg tccttatttc gtctcatgac tcaagacttc
1260 tggaaaaacc tttatcaact gacactacgt gctgctggga aaacgtacat gatattttt
1320 gtgctggtca ttttcttggg ctcattctat ctaataaatt tgatcttggc tgtggggcc
1380 atggcctatg aggaacagaa tcaggccaca ttggaagagg ctgaacagaa ggaagctgaa
1440 tttcagcaga tgctcgaaca gttaaaaag caacaagaag aagctcaggc ggcagctgca
1500 gcccgcacatctg ctgaatcaag agacttcagt ggtgctggtg ggataggagt ttttcagag
1560 agttcttcag tagcatctaa gttgagctcc aaaagtggaa aagagctgaa aaacagaaga
1620 aagaaaaaaga aacagaaaaga acagtctggaa gaagaagaga aaaatgacag agtcctaaaa
1680

SequencesSSCPRe-file7August03.ST25.txt

tcggaatctg aagacagcat aagaagaaaa ggttccgtt tttccttgg a g g a a g t a g g
1740

ctgacatatg aaaagagatt ttcttctcca caccagtct tactgagcat ccgtggctcc
1800

c t t t t c t c a a g a c g c a a c a g t a g g g c g a g c t t t c a g t a g g
1860

gacattggct ctgagaatga c t t t g c t g a t g a t g a c a g a c a a t g a c
1920

a g c c g a a g a g a c t c t c t g t t c g t g c a c a g a c a t g g a g a a c g c c a
1980

a g c c a g g c c a g c g c t c a g g g t g c t c c c c a t c c t g c a t g a a t g g
2040

a g c g c t g t g g a c t g c a a t g g t g g t c t c c t g g t c g g g g c c c t t c t a c
2100

g c t g g g c a g c t c t a c c a a c a c t a c t g a a a c a g a a a g a g a c g g t c c
2160

a g t t c t t a t c a t g t t c c a t g g a t t a t t g a a g a t c c t a c a t g a a g
2220

a g t a t a g c c a g t t t g a c a a c c a t g a a g a a c t t g a a g a t c c a g a
2280

c c a c c a t g c t g g a t t a t t g a a g a t c c t a c t g g a t t g g a c t g t t g
2340

t t a a a g g t g a a a c a c c t t g t c a a c c t g g t t g a a t g g a c c a t
2400

a c c a t c t g c a t t g t t a a a t a c a c t c t c a t g g c t a t g g a g
2460

c a g t t c a g c a g t g t c t g g a a a c c t g t t c a c a g g a t c t t c a c
2520

a t g t t c t c a a g a t t a t t g c a t g g a t c c a t t a t t a c t t c a a g
2580

t t t g a t g g t t t a t t g t g a g c c t t a a t g g a a c t t g g a a g g a
2640

t t g t c a g t t c t c c g g c t g c t c a g g t t t c a a g t t g g c a a a a t c t
2700

a c t c t a a a t a t a g c t a a t t a a g t c a t t g g c a a g g c t c t a g g
2760

SequencesSSCPRe-file7August03.ST25.txt
ttggtattgg ccatcatcg ttcatttt gctgtggtcg gcatgcagct cttggtaag
2820
agctacaaag aatgtgtctg caagattcc aatgattgtg aactcccacg ctggcacatg
2880
catgactttt tccactcctt cctgatcg tccgcgtgc tgtgtggaga gtggatagag
2940
accatgtggg actgtatgga gtcgctggc caaaccatgt gccttactgt cttcatgatg
3000
gtcatggta ttggaaatct agtggttctg aacctttct tggccttgct tttgagttcc
3060
ttcagttctg acaatcttgc tgccactgat gatgataacg aaatgaataa tctccagatt
3120
gctgtggaa ggatgcagaa aggaatcgat tttttaaaa gaaaaatacg tgaatttatt
3180
cagaaagcct ttgttaggaa gcagaaagct ttagatgaaa ttaaaccgct tgaagatcta
3240
aataataaaa aagacagctg tatttccaac cataccacca tagaaatagg caaagacctc
3300
aattatctca aagacggaaa tggaaactact agtggcatag gcagcagtgt agaaaaatata
3360
gtcgtggatg aaagtgatta catgtcattt ataaacaacc ctgcctcac tgtgacagta
3420
ccaattgctg ttggagaatc tgactttgaa aatttaaata ctgaagaatt cagcagcgag
3480
tcagatatgg aggaaagcaa agagaagcta aatgcaacta gttcatctga aggcagcacg
3540
gttgatattg gagctccgc cgagggagaa cagcctgagg ttgaacctga ggaatccctt
3600
gaacctgaag cctgtttac agaagactgt gtacggaagt tcaagtgttg tcagataagc
3660
ataagaagaag gcaaaggaa actctggtgg aatttgagga aagcatgcta taagatagtg
3720
gagcacaatt gttcgaaac cttcattgtc ttcatgattc tgctgagcag tggggctctg
3780
gccttgaag atatatacat tgagcagcga aaaaccatta agaccatgtt agaatatgct
3840
gacaaggttt tcacttacat attcattctg gaaatgctgc taaagtgggt tgcatatgg

SequencesSSCPRe-file7August03.ST25.txt

3900

tttcaagtgt attttaccaa tgcctgggc tggcttagact tcctgattgt tgatgtctca
3960

ctggtagct taactgcaaa tgcctgggt tactcagaac ttggtgccat caaatccctc
4020

agaacactaa gagctctgag gccactgaga gcttgcgg ggtttgaagg aatgagggtt
4080

gttgtaaatg ctcttttagg agccattcca tctatcatga atgtacttct gtttgcgt
4140

atctttggc taatatttcag tatcatggga gtgaatctct ttgctggcaa gtttaccat
4200

tgtattaatt acaccactgg agagatgtt gatgtaagcg tggtaaccaa ctacagttag
4260

tgcaaagctc tcattgagag caatcaaact gccaggtgga aaaatgtgaa agtaaacttt
4320

gataacgtag gacttggata tctgtctcta cttcaagtag ccacgtttaa gggatggatg
4380

gatattatgt atgcagctgt tgattcacga aatgtagaat tacaacccaa gtatgaagac
4440

aacctgtaca tgtatctta tttgtcatc tttattatgt ttggttcatt cttaaccttg
4500

aatctttca ttgggtcat catagataac ttcaaccaac agaaaaagaa gtttggaggt
4560

caagacattt ttatgacaga agaacagaag aaatactaca atgcaatgaa aaaactgggt
4620

tcaaagaaac cacaaaaacc catacctcga cctgctaaca aattccaagg aatggtctt
4680

gattttgtaa ccaaacaagt ctgtatc agcatcatga tcctcatctg ctttaacatg
4740

gtcaccatga tggtgaaac cgatgaccag agtcaagaaa tgacaaacat tctgtactgg
4800

attaatctgg tttttatgt tctgttcact ggagaatgtg tgctgaaact gatctcttt
4860

cgttactact atttcactat tggatgaaat attttgatt ttgtgggtt cattctctcc
4920

atgttaggaa tttttctggc tgaactgata gaaaagtatt ttgtgtcccc taccctgttc
4980

SequencesSSCPRe-file7August03.ST25.txt

cgagtgatcc gtcttgcag gattggccga atcctacgtc tgatcaaagg agcaaagggg
5040

atccgcacgc tgctcttgc tttgatgatg tcccttcctg cgttgttaa catggcctc
S100 .

cttctttcc tggcatgtt catctacgcc atcttggga tgtccaattt tgccatgttt
5160

aagagggaag ttgggatcga tgacatgttc aactttgaga cctttggcaa cagcatgatc
5220

tgcctgttcc aaattacaac ctctgctggc tggatggat tgctagcacc tattcttaat
5280

agtggacctc cagactgtga ccctgacaaa gatcaccctg gaagctcagt taaaggagac
5340

tgtggaaacc catctgttgg gatttcttt tttgtcagtt acatcatcat atccttcctg
5400

gttgtgctga acatgtacat cgccgtcatc ctggagaact tcagtgtgc tactgaagaa
5460

agtgcagagc ctctgagtga ggatgacttt gagatgttct atgaggtttggagaagttt
5520

gatcccgtg cgaccaggat tatagagttt gccaaacttt ctgattttgc agatgccctg
5580

gatccttcctc ttctcatagc aaaacccaac aaagtccagc tcattgccat ggatctgccc
5640

atggtgagtg gtgaccggat ccactgtctt gacatcttat ttgctttac aaagcgtgtt
5700

ttgggtgaga gtggagagat ggatgccctt cgaatacaga tggaaagagcg attcatggca
5760

tcaaacccct ccaaagtctc ttatgagccc attacgacca cggtgaaacg caaacaagag
5820

gaggtgtctg ctattattat ccagaggct tacagacgt acctcttgaa gaaaaagtt
5880

aaaaaggtat caagtatata caagaaagac aaaggcaaag aatgtgatgg aacacccatc
5940

aaagaagata ctctcattga taaactgaat gagaattcaa ctccagagaa aaccgataatg
6000

acgccttcca ccacgtctcc accctcgat gatagtgtga ccaaaccaga aaaagaaaaa
6060

SequencesSSCPRe-file7August03.ST25.txt

tttgaaaaag acaaatcaga aaaggaagac aaaggaaaag atatcaggggaaatggaaaag
6120

taaaaagaaa ccaagaattt tccatTTTgt gatcaattgt ttacagccccg tgatgggtgat
6180

gtgtttgtgt caacaggact cccacaggag gtctatgccaa actgactgt ttttacaaat
6240

gtatacttaa ggtcagtgc tataacaaga cagagacctc tggtcagcaa actggaaactc
6300

agtaaactgg agaaatagta tcgatggg
6328

<210> 6

<211> 6328

<212> DNA

<213> Homo sapiens

<400> 6

ttcttgggtgc cagcttatca atcccaaact ctgggtgtaa aagatttctac agggacttt
60

cttatgcaag gagctaaaca gtgattaaag gagcaggatg aaaagatggc acagtcagtg
120

ctggtaaccgc caggacctga cagcttccgc ttctttacca ggaaatccct tgctgctatt
180

gaacaacgca ttgcagaaga gaaagctaag agacccaaac aggaacgcaa ggatgaggat
240

gataaaaatg gcccaaagcc aaacagtgc ac ttggaaagcag gaaaatctct tccatttatt
300

tatggagaca ttcctccaga gatgggtgtca gtgccttgg aggatctgga cccctactat
360

atcaataaga aaacgtttat agtattgaat aaaggaaaag caatctctcg attcagtgc
420

accctgccc tttacatttt aactcccttc aaccctatta gaaaatttagc tattaagatt
480

ttggcacatt ctatttacaa tatgctcatt atgtgcacga ttcttacca ctgtgtattt
540

atgaccatga gtaaccctcc agactggaca aagaatgtgg agtataaccc tacaggaatt
600

tatacttttg aatcacttat taaaatactt gcaagggct tttgttttaga agatccaca
660

SequencesSSCPRe-file7August03.ST25.txt
tttttacggg atccatggaa ttgggttggat ttcacagtca ttactttgc atatgtgaca
720
gagtttgtgg acctggcaa tgtctcagcg ttgagaacat tcagagttct ccgagcattg
780
aaaacaattt cagtcattcc aggccctgaag accattgtgg gggccctgat ccagtcagtg
840
aagaagcttt ctgatgtcat gatcttgact gtgttctgtc taagcgtgtt tgcgctaata
900
ggattgcagt tgttcatggg caacctacga aataaatgtt tgcaatggcc tccagataat
960
tcttcctttg aaataaatat cacttccttc tttaacaatt cattggatgg gaatggtaact
1020
actttcaata ggacagttag catatccaac tggatgaat atattgagga taaaagtcac
1080
ttttatTTT tagagggca aaatgtatgt ctgcTTTGT gcaacagctc agatgcaggc
1140
cagtgtcctg aaggatacat ctgtgtgaag gctggtagaa accccaacta tggctacacg
1200
agctttgaca ccttagttg ggccttttg tccttatttc gtctcatgac tcaagacttc
1260
tggaaaaacc ttatcaact gacactacgt gctgctggga aaacgtacat gatatTTT
1320
gtgctggta ttttcttggg ctcattctat ctaataaatt tgatctggc tgggtggcc
1380
atggcctatg aggaacagaa tcaggccaca ttggaagagg ctgaacagaa ggaagctgaa
1440
tttcagcaga tgctcgaaca gttgaaaaag caacaagaag aagctcaggc ggcagctgca
1500
gccgcatttg ctgaatcaag agacttcagt ggtgctggtg ggataggagt ttttcagag
1560
agttcttcag tagcatctaa gttgagctcc aaaagtgaaa aagagctgaa aaacagaaga
1620
aagaaaaaga aacagaaaaga acagtctgga gaagaagaga aaaatgacag agtcctaaaa
1680
tcggaatctg aagacagcat aagaagaaaa ggttccgtt tttccttggg aggaagtagg
1740
ctgacatatg aaaagagatt ttcttcctcc caccagtcct tactgagcat ccgtggctcc

SequencesSSCPRe-file7August03.ST25.txt

1800

cttttctctc caagacgcaa cagtagggcg agcctttca gtttcagagg tcgagcaaag
1860

gacattggct ctgagaatga ctttgctgtat gatgagcaca gcaccttga ggacaatgac
1920

agccgaagag actctctgtt cgtgccgcac agacatggag aacggcgcca cagcaatgtc
1980

agccaggcca gccgtgcctc cagggtgctc cccatcctgc ccatgaatgg gaagatgcat
2040

agcgctgtgg actgcaatgg tgtggtctcc ctggtcgggg gcccttctac cctcacatct
2100

gctgggcage tcctaccaga gggcacaact actgaaacag aaataagaaa gagacggtcc
2160

agtctttatc atgtttccat ggatttattt gaagatccta catcaaggca aagagcaatg
2220

agtatagcca gtatTTTgac caacaccatg gaagaacttg aagaatccag acagaaatgc
2280

ccaccatgct ggtataaatt tgctaataatg ttttgattt gggactgttg taaaccatgg
2340

ttaaaggta aacacccgtt caacctggtt gtaatggacc catttggtaa cctggccatc
2400

accatctgca ttgtcttaaa tacactcttc atggctatgg agcactatcc catgacggag
2460

cagttcagca gtgtactgtc tttggaaac ctggcttca cagggatctt cacagcagaa
2520

atgtttctca agataattgc catggatcca tattattact ttcaagaagg ctggatatt
2580

tttgatggtt ttattgttag ctttagttt atgaaacttg gtttggcaaa tgtggaaagg
2640

ttgtcagttc tccgatcatt ccggctgctc cgagtttca agttggcaaa atcttggcca
2700

actctaaata tgctaattaa gatcattggc aattctgtgg gggctctagg aaacctcacc
2760

tttgttattgg ccatcatgt cttcattttt gctgtggtcg gcatgcagct ctttggtaag
2820

agctacaaag aatgtgtctg caagatttcc aatgattgtg aactcccacg ctggcacatg
2880

SequencesSSCPRe-file7August03.ST25.txt

catgacttt tccactcctt cctgatcgta ttccgcgtgc tgtgtggaga gtggatagag
2940

accatgtggg actgtatgga ggtcgctggc caaaccatgt gccttactgt ctcatgatg
3000

gtcatggta ttggaaatct agtggttctg aacctttct tggccttgct tttgagttcc
3060

ttcagttctg acaatcttgc tgccactgtat gatgataacg aaatgaataa tctccagatt
3120

gctgtggaa ggatgcagaa aggaatcgat tttgtaaaaaaa gaaaaatacg tgaatttatt
3180

cagaaaggct ttgttaggaa gcagaaagct ttagatgaaa ttaaaccgct tgaagatcta
3240

aataataaaaaa aagacagctg tatttccaac cataccacca tagaaatagg caaagacctc
3300

aattatctca aagacggaaa tggactact agtggcatag gcagcagtgt agaaaaataat
3360

gtcgtggatg aaagtgatta catgtcattt ataaacaacc ctgcctcac tgtgacagta
3420

ccaattgctg ttggagaatc tgactttgaa aatttaataa ctgaagaatt cagcagcgg
3480

tcagatatgg aggaaagcaa agagaagcta aatgcaacta gttcatctga aggcagcag
3540

gttgatattg gagctcccgc cgagggagaa cagcctgagg ttgaacctga ggaatccctt
3600

gaacctgaag cctgtttac agaagactgt gtacggaagt tcaagtgttg tcagataagc
3660

atagaagaag gcaaaggaa actctggtgg aatttgagga aaacatgcta taagatagt
3720

gagcacaatt ggttcgaaac cttcattgtc ttcatgattc tgctgagcag tggggctctg
3780

gccttgaag atatatacat tgagcagcga aaaaccatta agaccatgtt agaatatgct
3840

gacaaggttt tcacttacat attcattctg gaaatgctgc taaagtgggt tgcatatgg
3900

tttcaagtgt attttaccaa tgcctggtgc tggcttagact tcctgattgt tgatgtctca
3960

SequencesSSCPRe-file7August03.ST25.txt
ctggtagct taactcaaa tgcctgggt tactcagaac ttgggccat caaatccctc
4020
agaacactaa gagctctgag gccactgaga gcttgcggc agtttgaagg aatgagggtt
4080
gttgtaatg ctctttagg agccattcca tctatcatga atgtacttct gtttgcgg
4140
atctttggc taatattcag tatcatggg gtgaatctt ttgctggcaa gtttaccat
4200
tgtattaatt acaccactgg agagatgtt gatgtaagcg tggtaaccaa ctacagttag
4260
tgcaagctc tcattgagag caatcaaact gccaggtgga aaaatgtgaa agtaaacttt
4320
gataacgtag gacttggata tctgtctcta cttcaagtag ccacgtttaa gggatggatg
4380
gatattatgt atgcagctgt tgattcacga aatgtagaat tacaacccaa gtatgaagac
4440
aacctgtaca tgtatctta tttgtcatc tttattattt ttggttcatt cttaccttg
4500
aatctttca ttgggtcat catagataac ttcaaccaac agaaaaagaa gtttggaggt
4560
caagacattt ttatgacaga agaacagaag aaatactaca atgcaatgaa aaaactgggt
4620
tcaaagaaac cacaaaaacc catacctcg a ctcgtaaca aattccaagg aatggtctt
4680
gatttgtaa ccaaacaagt ctttgatatc agcatcatga tcctcatctg ctttaacatg
4740
gtcaccatga ttgggaaac cgatgaccag agtcaagaaa tgacaaacat tctgtactgg
4800
attaatctgg tgtttattgt tctgttcact ggagaatgtg tgctgaaact gatctctt
4860
cgtttactat atttcaactat tggatgaaat attttgatt ttgtgggtt cattctctcc
4920
atgttagaa tgtttctggc tgaactgata gaaaagtatt ttgtgtcccc taccctgttc
4980
cgagtgatcc gtcttgcag gatggccga atcctacgtc tgatcaaagg agcaaagggg
5040
atccgcacgc tgctcttgc tttgatgatg tcccttcctg cgttggtaa catggccctc

SequencesSSCPRe-file7August03.ST25.txt

5100

cttctttcc tggcatgtt catctacgcc atcttgga tgtccaattt tgccatgtt
5160

aagagggaaag ttggatcga tgacatgttc aacttgaga ctttggcaa cagcatgatc
5220

tgcctgtcc aaattacaac ctctgctggc tggatggat tgctagcacc tattcttaat
5280

agtggaccc cagactgtga ccctgacaaa gatcacccctg gaagctcagt taaaggagac
5340

tgtggaaacc catctgttg gatttctt tttgtcagtt acatcatcat atccttcctg
5400

gttgtgctga acatgtacat cgccgtcata ctggagaact tcagtgtgc tactgaagaa
5460

agtgcagagc ctctgagtga ggatgactt gagatgtct atgaggtttg ggagaagtt
5520

gatcccgtcg cacccagtt tatagagttt gccaaacttt ctgatttgc agatgccctg
5580

gatcctcctc ttctcatagc aaaaccaac aaagtccagc tcattgccat ggatctgccc
5640

atggtgagtg gtgaccggat ccactgtctt gacatcttac ttgctttac aaagcgtgtt
5700

ttgggtgaga gtggagagat ggatgccctt cgaatacaga tggaaagagcg attcatggca
5760

tcaaaccctt ccaaagtctc ttatgagccc attacgacca cgttgaaacg caaacaagag
5820

gaggtgtctg ctattattat ccagaggct tacagacgt acctttgaa gaaaaagtt
5880

aaaaaggtat caagtatata caagaaagac aaaggcaaag aatgtgatgg aacacccatc
5940

aaagaagata ctctcattga taaactgaat gagaattcaa ctccagagaa aaccgatatg
6000

acgccttcca ccacgtctcc accctcgat gatagtgtga ccaaaccaga aaaaagaaaa
6060

tttggaaaaag acaaattcaga aaaggaagac aaaggaaag atatcaggaa aagtaaaaag
6120

taaaaaagaaa ccaagaattt tccatttgt gatcaattgt ttacagcccc tgatgggtat
6180

SequencesSSCPRe-file7August03.ST25.txt

gtgtttgtgt caacaggact cccacaggag gtctatgcca aactgactgt ttttacaaat
6240

gtatacttaa ggtcagtgcc tataacaaga cagagacctc tggtcagcaa actggaaactc
6300

agtaaaactgg agaaaatagta tcgatggg
6328

<210> 7
<211> 6328
<212> DNA
<213> Homo sapiens

<400> 7
ttcttggtgc cagcttatca atcccaaact ctgggtgtaa aagattctac agggcactt
60

cttatgcaag gagctaaaca gtgattaaag gagcaggatg aaaagatggc acagtcagtg
120

ctggtaaccgc caggacctga cagcttccgc ttctttacca ggaaatccct tgctgttatt
180

gaacaacgca ttgcagaaga gaaagctaag agacccaaac aggaacgcaa ggatgaggat
240

gataaaaatg gcccaaagcc aaacagtgac ttggaaagcag gaaaatctct tccatttatt
300

tatggagaca ttcctccaga gatgggtgtca gtgccttgg aggatctgga cccctactat
360

atcaataaga aaacgtttat agtattgaat aaaggaaag caatctctcg attcagtgcc
420

accctgccc tttacattt aactcccttc aaccctatta gaaaatttagc tattaagatt
480

ttggcacatt ctttattcaa tatgctcatt atgtcacga ttcttaccaa ctgtgttattt
540

atgaccatga gtaaccctcc agactggaca aagaatgtgg agtataccct tacaggaatt
600

tatacttttg aatcacttat taaaatactt gcaagggct tttgtttaga agatttcaca
660

tttttacggg atccatggaa ttgggtggat ttcacagtca ttactttgc atatgtaca
720

gagtttgcgg acctggcaa tgtctcagcg ttgagaacat tcagagttct ccgagcattg
780

SequencesSSCPRe-file7August03.ST25.txt

aaaacaattt cagtcattcc aggcctgaag accattgtgg gggccctgat ccagtcagtg
840

aagaagcttt ctgatgtcat gatcttgact gtgttctgtc taagcgtgtt tgcgctaata
900

ggattgcagt ttttcatggg caacctacga aataaatgtt tgcaatggcc tccagataat
960

tcttccttg aaataaat cacttccttc tttaacaatt cattggatgg gaatggtaact
1020

actttcaata ggacagttag catatttaac tggatgaat atattgagga taaaagtcac
1080

ttttatttt tagagggca aaatgtatgt ctgctttgtg gcaacagctc agatgcaggc
1140

cagtgtcctg aaggatacat ctgtgtgaag gctggtagaa acccaacta tggctacacg
1200

agctttgaca ccttagttt ggccttttg tccttatttc gtctcatgac tcaagacttc
1260

tggaaaaacc tttatcaact gacactacgt gctgctgggaa aaacgtacat gatatTTTT
1320

gtgctggtaa ttttcttggg ctcattctat ctaataaaatt tgatcttggc tgggtggcc
1380

atggcctatg aggaacagaa tcaggccaca ttggaaagagg ctgaacagaa ggaagctgaa
1440

tttcagcaga tgctcgaaca gttaaaaaag caacaagaag aagctcaggc ggcagctgca
1500

gccgcatctg ctgaatcaag agacttcagt ggtgctggtg ggataggagt ttttcagag
1560

agtcttcag tagcatctaa gttgagctcc aaaagtggaa aagagctgaa aaacagaaga
1620

aagaaaaaaga aacagaaaaga acagtctgga gaagaagaga aaaatgacag agtcctaaaa
1680

tcgaaatctg aagacagcat aagaagaaaa ggtttccgtt tttccttggg aggaaagttagg
1740

ctgacatatg aaaagagatt ttcttctcca caccagtcct tactgagcat ccgtggctcc
1800

cttttcttc caagacgcaa cagtagggcg agcctttca gtttcagagg tcgagcaaag
1860

SequencesSSCPRe-file7August03.ST25.txt

gacattggct ctgagaatga ctttgctgac gatgagcaca gcaccttga ggacaatgac
1920

agccgaagag actctctgtt cgtgccgcac agacatggag aacggcgcca cagcaatgtc
1980

agccaggcca gccgtgcctc cagggtgctc cccatcctgc ccatgaatgg gaagatgcat
2040

agcgctgtgg actgcaatgg tgtggctcc ctggtcgggg gcccttctac cctcacatct
2100

gctgggcage tcctaccaga gggcacaact actgaaacag aaataagaaa gagacggtcc
2160

agtcttatac atgtttccat ggatttattt gaagatccta catcaaggca aagagcaatg
2220

agtatagcca gtatTTGAC caacaccatg gaagaacttg aagaatccag acagaaatgc
2280

ccaccatgct ggtataaaatt tgctaataatg tgTTTgattt gggactgttg taaaccatgg
2340

ttaaaggta aacaccttgt caacctgggt gtaatggacc catttggta cctggccatc
2400

accatctgca ttgtcttaaa tacacttttc atggctatgg agcactatcc catgacggag
2460

cagttcagca gtgtactgtc tgTTGAAAC ctggcttca cagggatctt cacagcagaa
2520

atgtttctca agataattgc catggatcca tattattact ttcaagaagg ctggaatatt
2580

tttgatggtt ttattgttag ccttagttt atgaaacttg gtttggcaaa tgtggagga
2640

ttgtcagttc tccgatcatt ccggctgctc cgagTTTca agttggcaaa atcttggcca
2700

actctaaata tgctaattaa gatcattggc aattctgtgg gggctctagg aaacctcacc
2760

tttgtattgg ccatcatcgt cttcattttt gctgtggtcg gcatgcagct ctttggtaag
2820

agctacaaag aatgtgtctg caagatttcc aatgattgtg aactcccacg ctggcacatg
2880

catgactttt tccactcatt cctgatcgtg ttccgcgtgc tgtgtggaga gtggatagag
2940

accatgtggg actgtatgga ggtcgctggc caaaccatgt gccttactgt cttcatgatg

SequencesSSCPRe-file7August03.ST25.txt

3000 gtcatggta ttggaaatct agtggttctg aacctttct tggccttgct tttgagttcc
3060 ttcagttctg acaatcttgc tgccactgtat gatgataacg aaatgaataa tctccagatt
3120 gctgtggaa ggatgcagaa aggaatcgat tttgttaaaa gaaaaatacg tgaatttatt
3180 cagaaaggcct ttgttaggaa gcagaaagct ttagatgaaa ttaaaccgct tgaagatcta
3240 aataataaaa aagacagctg tatttccaac cataccacca tagaaatagg caaagacctc
3300 aatttatctca aagacggaaa tggactact agtggcatag gcagcagtgt agaaaaatat
3360 gtcgtggatg aaagtgatta catgtcattt ataaacaacc ctgcctcac tgtgacagta
3420 ccaattgctg ttggagaatc tgactttgaa aatttaaata ctgaagaatt cagcagcgag
3480 tcagatatgg aggaaagcaa agagaagcta aatgcaacta gttcatctga aggcagcacg
3540 gttgatattg gagctccgc cgagggagaa cagcctgagg ttgaacctga ggaatccctt
3600 gaacctgaag cctgtttac agaagactgt gtacggaagt tcaagtgttgcagataagc
3660 atagaagaag gcaaaggaa actctggtgg aatttgagga aaacatgcta taagatagt
3720 gagcacaatt ggtcgaaac cttcattgtc ttcatgattc tgctgagcag tggggctctg
3780 gccttgaag atatatacat tgagcagcga aaaaccatta agaccatgtt agaatatgct
3840 gacaagggtt tcacttacat attcattctg gaaatgctgc taaagtgggt tgcatatgg
3900 ttcaagtgt attttaccaa tgcctggtgc tggctagact tcctgattgt tgatgtctca
3960 ctggtagct taactgcaaa tgcctgggt tactcagaac ttggtgccat caaatccctc
4020 agaacactaa gagctctgag gccactgaga gctttgtccc gggttgaagg aatgagggtt
4080

SequencesSSCPRe-file7August03.ST25.txt

gttgtaaatg ctcttttagg agccattcca tctatcatga atgtacttct ggtttgtctg
4140

atctttggc taatattcag tatcatgggaa gtgaatctct ttgctggcaa gttttaccat
4200

tgtattaatt acaccactgg agagatgttt gatgttaagcg tggtaacaa ctacagttag
4260

tgcaagctc tcattgagag caatcaaact gccagggtgaa aaaatgtgaa agtaaaacttt
4320

gataacgtag gacttggata tctgtctcta cttcaagtag ccacgtttaa gggatggatg
4380

gatattatgt atgcagctgt tgattcacga aatgtagaat tacaacccaa gtatgaagac
4440

aacctgtaca tgtatcttta ttttgtcatc tttattattt ttggttcatt ctttaccttg
4500

aatctttca ttgggtgtcat catagataac ttcaaccaac agaaaaagaa gtttggaggt
4560

caagacattt ttatgacaga agaacagaag aaatactaca atgcaatgaa aaaactgggt
4620

tcaaagaaac cacaaaaacc catacctcga cctgctaaca aattccaagg aatggtcttt
4680

gattttgtaa ccaaacaagt ctttgatatac agcatcatga tcctcatctg ccttaacatg
4740

gtcaccatga tggtgaaac cgatgaccag agtcaagaaa tgacaaacat tctgtactgg
4800

attaatctgg tgtttattgt tctgttcact ggagaatgtg tgctgaaact gatctcttt
4860

cgttactact atttcactat tggatggaa attttgatt ttgtgggtt cattctctcc
4920

attgttagaa tgtttctggc tgaactgata gaaaagtatt ttgtgtcccc taccctgttc
4980

cgagtgatcc gtcttgcag gattggccga atcctacgtc tgatcaaagg agcaaagggg
5040

atccgcacgc tgctcttgc tttgatgatg tcccttcctg cgttgtttaa catggcctc
5100

cttctttcc tggcatgtt catctacgcc atcttggaa tgtccaaattt tgcctatgtt
5160

SequencesSSCPRe-file7August03.ST25.txt
aagagggaag ttgggatcga tgacatgttc aacttgaga cctttggcaa cagcatgatc
5220
tgccctgttcc aaattacaac ctctgctggc tgggatggat tgcttagcacc tattcttaat
5280
agtggaccc tcagactgtga ccctgacaaa gatcaccctg gaagctcagt taaaggagac
5340
tgtgggaacc catctgttgg gattttctt tttgtcagtt acatcatcat atccttcctg
5400
gttgtgctga acatgtacat cgcggtcatc ctggagaact tcagtgtgc tactgaagaa
5460
agtgcagagc ctctgagtga ggatgacttt gagatgttct atgaggtttg ggagaagttt
5520
gatcccgtat cgaccaggat tatagagttt gccaaacttt ctgattttgc agatgccctg
5580
gatecttcctc ttctcatagc aaaacccaac aaagtccagc tcattgccat ggatctgccc
5640
atggtgagtg gtgaccggat ccactgtctt gacatcttat ttgctttac aaagcgtgtt
5700
ttgggtgaga gtggagagat ggatgccctt cgaatacaga tggaaagagcg attcatggca
5760
tcaaaccctt ccaaagtctc ttatgagccc attacgacca cgttgaaacg caaacaagag
5820
gaggtgtctg ctattattat ccagaggct tacagacgct acctcttcaa gcaaaaaagtt
5880
aaaaaggtat caagtatata caagaaagac aaaggcaaag aatgtgatgg aacacccatc
5940
aaagaagata ctctcattga taaactgaat gagaattcaa ctccagagaa aaccgatatg
6000
acgccttcca ccacgtctcc accctcgat gatagtgtga ccaaaccaga aaaagaaaaa
6060
tttggaaaaag acaaattcaga aaaggaagac aaagggaaag atatcaggaa aagtttttttt
6120
taaaaaagaaa ccaagaattt tccattttgt gatcaattgt ttacagccccg tggatggat
6180
gtgtttgtgtt caacaggact cccacaggag gtctatgcca aactgactgt ttttacaaat
6240
gtataacttaa ggtcagtgcc tataacaaga cagagaccc tcggtcagcaa actggaaactc

6300

SequencesSSCPre-file7August03.ST25.txt

agtaaaactgg agaaaatagta tcgatggg
6328

<210> 8
<211> 6328
<212> DNA
<213> Homo sapiens

<400> 8
ttcttggtgc cagcttatca atcccaaact ctgggtgtaa aagattctac agggcacttt
60

cttatgcaag gagctaaaca gtgattaaag gagcaggatg aaaagatggc acagtca
120

ctggtaccgc caggacctga cagcttccgc ttctttacca gggaaatccct tgctgctatt
180

gaacaacgca ttgcagaaga gaaagctaag agacccaaac aggaacgcaa ggatgaggat
240

gataaaaatg gcccaaagcc aaacagtgc ac ttggaaagcag gaaaatctct tccatttatt
300

tatggagaca ttcctccaga gatggtgtca gtgccttgg aggatctgga cccctactat
360

atcaataaga aaacgtttat agtattgaat aaaggaaag caatctctcg attcagtgcc
420

accctgccc tttacattt aactcccttc aaccctatta gaaaatttagc tattaagatt
480

tttgtacatt cttaattcaa tatgctcatt atgtgcacga ttcttacca ctgtgtattt
540

atgaccatga gtaaccctcc agactggaca aagaatgtgg agtatacctt tacaggaatt
600

tatacttttg aatcacttat taaaatactt gcaaggggct tttgtttaga agatttcaca
660

tttttacggg atccatggaa ttgggtggat ttcacagtca ttactttgc atatgtgaca
720

gagtttggg acctggcaa tgtctcagcg ttgagaacat tcagagttct ccgagcattt
780

aaaacaattt cagtcattcc aggctgaag accattgtgg gggccctgat ccagtcagtg
840

aagaagcttt ctgatgtcat gatcttgcact gtgtctgtc taagcgtgtt tgctctaata

900

SequencesSSCPRe-file7August03.ST25.txt

ggattgcagt tgttcatggg caacctacga aataaatgtt tgcaatggcc tccagataat
960
tcttcctttg aaataaatat cacttccttc tttaacaatt cattggatgg gaatggtaact
1020
acttcaata ggacagttag catatttaac tggatgaat atattgagga taaaagtcac
1080
tttatTTTT tagagggca aaatgatgct ctgctttgtg gcaacagctc agatgcaggc
1140
cagtgtcctg aaggatacat ctgtgtgaag gctggtagaa accccaacta tggctacacg
1200
agctttgaca ccttagttg ggccttttg tccttatttc gtctcatgac tcaagacttc
1260
tggaaaaacc tttatcaact gacactacgt gctgctggga aaacgtacat gatatTTTT
1320
tgctggta tttcttggg ctcattctat ctaataaatt tgatcttggc tgtggggcc
1380
atggcctatg aggaacagaa tcaggccaca ttggaaaggagg ctgaacagaa ggaagctgaa
1440
ttcagcaga tgctcgaaca gttggaaaag caacaagaag aagctcaggc ggcagctgca
1500
gccgcattcg ctgaatcaag agacttcagt ggtgctggtg ggataggagt ttttcagag
1560
agtcttcag tagcatctaa gttgagctcc aaaagtggaa aagagctgaa aaacagaaga
1620
aagaaaaaga aacagaaaaga acagtctgga gaagaagaga aaaatgacag agtcctaaaa
1680
tcggaatctg aagacagcat aagaagaaaa gtttccgtt tttcttggg aggaagttagg
1740
ctgacatatg aaaagagatt ttcttctcca caccagtcc tactgagcat ccgtggctcc
1800
ctttctctc caagacgcaa cagtagggcg agcctttca gttcagagg tcgagcaaag
1860
gacattggct ctgagaatga ctttgctgat gatgagcaca gcaccttga ggacaatgac
1920
agccgaagag actctctgtt cgtgccgcac agacatggag aacggcgcca cagcaatgtc
1980

SequencesSSCPRe-file7August03.ST25.txt

agccaggcca gccgtgcctc cagggtgctc cccatcctgc ccatgaatgg gaagatgcat
2040
agcgctgtgg actgcaatgg tgtggtctcc ctggtcgggg gcccctctac cctcacatct
2100
gctgggcagc tcctaccaga gggcacaact actgaaacag aaataagaaa gagacggtcc
2160
agtctttatc atgtttccat ggatttattg gaagatccta catcaaggca aagagcaatg
2220
agtatagcca gtatTTGAC caacaccatg gaagaacttg aagaatccag acagaaatgc
2280
ccaccatgct ggtataaatt tgctaataatg tgTTTgattt gggactgttg taaaccatgg
2340
ttaaaggtga aacacCTTGT caacCTggTT gtaatggacc catttggTTga CCTggCCATC
2400
accatctgca ttgtctaaa tacactcttc atggctatgg agcactatcc catgacggag
2460
cagttcagca gtgtactgtc tgTTggAAAC ctggTcttca cagggatctt cacagcagaa
2520
atgtttctca agataattgc catggatcca tattattact ttcaagaagg ctggaatatt
2580
tttggatggTT ttattgtgag CCTtagTTA atggAACTTG gTTggCAAA TGTggAAGGA
2640
ttgtcagttc tccgatcatt ccggctgctc cgagTTTca agttggCAAA atcttggCCA
2700
actctaaata tgctaattaa gatcattggc aattctgtgg gggctctagg aaacctcacc
2760
tttgttattgg ccatcatcgt cttcatTTT gctgtggTCg gcatgcagct ctTTggtaag
2820
agctacaaag aatgtgtctg caagatttcc aatgattgtg aactcccacg ctggcacatg
2880
catgactttt tccactcctt cctgatcgtg ttccgcgtgc tgtgtggaga gtggatagag
2940
accatgtggg actgtatgga ggtcgctggc caaaccatgt gccttactgt ctTCatgatg
3000
gtcatggtgta ttggaaatct agtggTTctg aacctttct tggcTTgct tttgagttcc
3060

SequencesSSCPRe-file7August03.ST25.txt
ttcagttctg acaatcttgc tgccactgtat gatgataacg aaatgaataaa tctccagatt
3120
gctgtggaa ggatgcagaa aggaatcgat tttgttaaaa gaaaaatacg tgaatttatt
3180
cagaaagcct ttgttaggaa gcagaaagct ttagatgaaa ttaaaccgct tgaagatcta
3240
aataataaaa aagacagctg tatttccaac cataccacca tagaaatagg caaagacctc
3300
aatttatctca aagacggaaa tggactact agtggcatag gcagcagtgt agaaaaatata
3360
gtcgtggatg aaagtgatta catgtcattt ataaacaacc ctagcctcac tgtgacagta
3420
cقاattgctg ttggagaatc tgactttgaa aatttaataa ctgaagaatt cagcagcag
3480
tcagatatgg aggaaagcaa agagaagcta aatgcaacta gttcatctga aggcagcacg
3540
gttgatattg gagctccgc cgagggagaa cagcctgagg ttgaacctga ggaatccctt
3600
gaacctgaag cctgtttac agaagactgt gtacggaagt tcaagtgttgc tcaagataac
3660
atagaagaag gcaaaggaa actctggtgg aatttgagga aaacatgcta taagatagtg
3720
gagcacaatt ggtcgaaac cttcattgtc ttcatgattc tgctgagcag tgggctctg
3780
gcctttgaag atatatacat tgagcagcga aaaaccatta agaccatgtt agaatatgct
3840
gacaaggttt tcacttacat attcattctg gaaatgctgc taaagtgggt tgcatatgg
3900
tttcaagtgt attttaccaa tgcctggtgc tggctagact tcctgattgt tgatgtctca
3960
ctggtagct taactgcaaa tgcctgggt tactcagaac ttggtgccat caaatccctc
4020
agaacactaa gagctctgag gccactgaga gctttgtccc gtttgaagg aatgagggtt
4080
gttgtaaatg ctcttttagg agccattcca tctatcatga atgtacttct gtttggct
4140
atctttggc taatattcag tatcatggaa gtgaatctct ttgctggcaa gtttaccat

SequencesSSCPRe-file7August03.ST25.txt

4200

tgttataatt acaccactgg agagatgttt gatgttaagcg tggtaaccaa ctacagttag
4260

tgcaaagctc tcattgagag caatcaaact gccaggtgga aaaatgtgaa agtaaacttt
4320

gataacgtag gacttgata tctgtctcta cttcaagtag ccacgtttaa gggatggatg
4380

gatattatgt atgcagctgt tgattcacga aatgtagaat tacaacccaa gtatgaagac
4440

aacctgtaca tgtatcttta ttttgtcatc ttattttttt ttgggttcatt cttaaccctg
4500

aatctttca ttgggtgtcat catagataac ttcaaccaac agaaaaagaa gtttggaggt
4560

caagacattt ttatgacaga agaacagaag aaatactaca atgcaatgaa aaaactgggt
4620

tccaaaagaaac cacaaaaacc catacctcgat cctgctaaca aattccaagg aatggtcttt
4680

gattttgtaa ccaaacaagt ctttgatatac agcatcatga tcctcatctg ccttaacatg
4740

gtcaccatga tggggaaac cgatgaccag agtcaagaaa tgacaaacat tctgtactgg
4800

attaatctgg tggttatgtt tctgttcact ggagaatgtg tgctgaaact gatctcttt
4860

cgtttactat atttcactat tggatggaat atttttgatt ttgtggtggt cattctctcc
4920

attgttaggaa tggttctggc tgaactgata gaaaagtatt ttgtgtcccc taccctgttc
4980

cgagtgtatcc gtcttgccag gattggccga atccctacgtc tgaacaaaagg agcaaaagggg
5040

atccgcacgc tgctctttgc ttgtatgtatg tcccttcttg cgttgtttaa catcgccctc
5100

5160 tggtcatgtt catctacgcc acctttggga tgccaaattt tgcctatgtt

aaaggagggaag ttggggatcga tgatatgtttt aacttttgaga cctttggcaa cagcatgatc
5220

tcgttgcggc aaattacaac ctctgtggc tgggatggat tgcttagcacc tatttttaat
5280

SequencesSSCPRe-file7August03.ST25.txt

agtggaccc cagactgtga ccctgacaaa gatcaccctg gaagctcagt taaaggagac
5340

tgtggaaacc catctgttgg gatttcttt tttgtcagtt acatcatcat atccttcctg
5400

gttgtgctga acatgtacat cgcggtcatc ctggagaact tcagtgtgc tactgaagaa
5460

agtgcagagc ctctgagtga ggatgacttt gagatgttct atgaggtttg ggagaagttt
5520

gatcccgtg cgaccaggatt tatagagttt gccaaacttt ctgattttgc agatgccctg
5580

gatecttcctc ttctcatagc aaaacccaac aaagtccagc tcattgccat ggatctgccc
5640

atggtgagtg gtgaccggat ccactgtctt gacatcttat ttgctttac aaagcgtgtt
5700

ttgggtgaga gtggagagat ggatgccctt cgaatacaga tggaaagagcg attcatggca
5760

tcaaaccctt ccaaagtctc ttatgagccc attacgacca cgttgaaacg caaacaagag
5820

gaggtgtctg ctattattat ccagaggct tacagacgct acctcttgc gcaaaaagtt
5880

aaaaaggtat caagtatata caagaaagac aaaggcaaag aatgtgatgg aacacccatc
5940

aaagaagata ctctcattga taaactgaat gagaattcaa ctccagagaa aaccgatatg
6000

acgccttcca ccacgtctcc accctcgat gatagtgtga ccaaaccaga aaaaagaaaa
6060

tttggaaaaag acaaattcaga aaaggaagac aaagggaaag atatcagggg aagtaaaaag
6120

taaaaagaaa ccaagaattt tccatttgt gatcaattgt ttacagcccg tgatgggtat
6180

gtgtttgtgt caacaggact cccacaggag gtctatgcc aactgactgt ttttacaaat
6240

gtataactaa ggtcagtgcc tataacaaga cagagaccc tggtcagcaa actggaaactc
6300

agtaaaactgg agaaatagta tcgatggg
6328

SequencesSSCPRe-file7August03.ST25.txt

<210> 9
<211> 238
<212> DNA
<213> Homo sapiens

<400> 9
gtggaactcc agcctaagta tgaagaaagt ctgtacatgt atctttactt tgttatttc
60

atcatcttg ggtccttctt caccttgaac ctgtttatttgcgtcatcat agataatttc
120

aaccaggaga aaaagaagat aagtatttct aatattttct ctcactga aatagaaaaat
180

tattccttgg agtgtttctt ctgccaaatg agtacttcaa tttagaaaca aaatggga
238

<210> 10
<211> 373
<212> DNA
<213> Homo sapiens

<400> 10
gcctgaagac cattgtgggg gccctgatcc agtcagtgaa gaagctttctt gatgtcatga
60

tcttgactgt gttctgtcta agcgtgtttcgctaatagg attgcagtttgcattggca
120

acctacgaaa taaatgttttgcattggcctc cagataatttgcattttgaa ataaatatca
180

cttccttctt taacaatttca ttggatggga atggtaactac ttcaatagg acagtggca
240

tatattaactg ggatgaatat attgaggata aaagtaagat atactctata aaccatata
300

ttgttttagtt ctctaaatat taaatattat ataaaatggaa aattatctca atttagatgt
360

gaatcaagtact
373

<210> 11
<211> 274
<212> DNA
<213> Homo sapiens

<400> 11
taggcacctg ataagagctt gcacgttttc cttttttaag aaatcgtaa tttagagactg

tttctgatca taaaatttaa tagaatttt tgacttacag gccttgaag atatatacat
120

tgagcagcga aaaaccatta agaccatgtt agaatatgct gacaagggtt tcacttacat
180

attcattctg gaaatgctgc taaagtgggt tgcataatggt tttcaagtgt attttaccaa
240

tgcctggtgc tggctagact tcctgattgt tgat
274

<210> 12

<211> 154

<212> DNA

<213> Homo sapiens

<400> 12

gtattgaata catgtcaaat agaatttga tcaattattc aatttatttt ctaaaattat
60

aattttgggg aaaaagaaaa tgatatgact ttcttacag gccacgtta agggatggat
120

ggatattatg tatgcagctg ttgattcacg aaat
154

<210> 13

<211> 219

<212> DNA

<213> Homo sapiens

<400> 13

ttacagggca atatttataa ataatggtt tactttctc ttaaaatatt cttaatataat
60

attctaagtt ttattttatg ttttgtttt tcttttcag acgtttatag tattgaataa
120

aggaaagca atctctcgat tcagtgccac ccctgccctt tacattttaa ctcccttcaa
180

ccctattaga aaatttagcta ttaagatttt ggtacattc
219

<210> 14

<211> 242

<212> DNA

<213> Homo sapiens

SequencesSSCPRe-file7August03.ST25.txt

<400> 14
gtgcctgtat aaaacagaca ttggcataata taaaaacagg aaaaccaatt agcagacttg
60

ccgttattga ctccctttct ttcctctaac ctaattacag ccagtgtcct gaaggataca
120

tctgtgtgaa ggctggtaga aaccccaact atggctacac gagcttgac accttttagtt
180

gggcctttt gtccttattt cgtctcatga ctcaagactt ctgggaaaac ctttatcaac
240

tg
242

<210> 15

<211> 388

<212> DNA

<213> Homo sapiens

<400> 15

gcggcagctg cagccgcattc tgctgaatca agagacttca gtggtgctgg tgggatagga
60

gtttttcag agagtttttc agtagcatct aagttgagct ccaaaagtga aaaagagctg
120

aaaaacagaa gaaagaaaaa gaaacagaaa gaacagtctg gagaagaaga gaaaaatgac
180

agagtcctaa aatcgaaatc tgaagacagc ataagaagaa aaggttccg ttttccttg
240

gaaggaagta ggctgacata tgaaaagaga ttttcttctc cacaccaggt aaaaatatta
300

aattacatga attgtgttct cataaatttt taaaaagaat atgccagaat ttaatggaga
360

gaaaaccgcc ttccacctgg atggcaca
388

<210> 16

<211> 445

<212> DNA

<213> Homo sapiens

<400> 16

aagtcaatga ctatgacaca atgaatcaaa ttctgtttt cagaatgcc a gctttaact
60

ctcttcatct cattttgtt tctttcttg ttattcatag tccttactga gcatccgtgg

120

SequencesSSCPRe-file7August03.ST25.txt

ctccctttc tctccaagac gcaacagttag ggcgagcctt ttcaagttca gaggtcgagc
180

aaaggacatt ggctctgaga atgactttgc tgatgtatgag cacagcacct ttgaggacaa
240

tgcacagccga agagactctc tgttcgtgcc gcacagacat ggagaacggc gccacagcaa
300

tgtcagccag gccagccgtg cctccagggt gctccccatc ctgcccattga atggaaagat
360

gcatacgct gtggactgca atggtgtggt ctccctggtc gggggccctt ctaccctcac
420

atctgctggg cagctcctac cagag
445

<210> 17

<211> 221

<212> DNA

<213> Homo sapiens

<400> 17

aaatgcatac agaagatggg gggggggcat acctaattaa ttttatatt tagattaaag
60

aaaataatta aatgtgtttt tttgtggat tgatttcag aagctaaatg caactagttc
120

atctgaaggc agcacggttg atattggagc tcccgccgag ggagaacacgc ctgaggttga
180

acctgaggaa tcccttgaac ctgaaggctg ttttacagaa g
221

<210> 18

<211> 221

<212> DNA

<213> Homo sapiens

<400> 18

aaaatgcata cagaagatgg gggggggcac acctaattaa ttttatatt tagattaaag
60

aaaataatta aatgtgtttt tttgtggat tgatttcag aagctaaatg caactagttc
120

atctgaaggc agcacggttg atattggagc tcccgccgag ggagaacacgc ctgaggttga
180

SequencesSSCPRe-file7August03.ST25.txt
acctgaggaa tcccttgaac ctgaagcctg ttttacagaa g
221

<210> 19
<211> 221
<212> DNA
<213> Homo sapiens

<400> 19
aatgcataca gaagatgggg gggggggcac acctaattaa ttttatatt tagattaaag
60

aaaataatta aatgtgttt tttgtggat tgatttcag aagctaaatg caactagttc
120

atctgaaggc agcacggttg atattggagc tcccgccgag ggagaacagc ctgagggtga
180

acctgaggaa tcccttgaac ctgaagcctg ttttacagaa g
221

<210> 20
<211> 1679
<212> DNA
<213> Homo sapiens

<400> 20
gggagctgtg gcgcggagcg gcccctctgc tgctgtgcc ctcttttgt ctcacgactc
60

acactcagtg ctccattccc caagagttcg cgccccccgc gcggcggtcg agaggcggct
120

gcccgcggtc ccgcgcgggc gcggggcgat ggcggcgcgg gggtcagggc cccgcgcgc
180

ccgcctgctg ctcttggtcc agctggtcgc gggggcgctg cggcttagcc gggcgcggcg
240

ggccgcgcgc agaggattat ctgaaccttc ttctattgca aaacatgaag atagtttgct
300

taaggattta ttcaagact acgaaagatg gtttcgtctt gtggAACACC tgaatgacaa
360

aataaaaata aaatttggac ttgcaatatc tcaattggtg gatgtggatg agaaaaatca
420

gttaatgaca acaaacgtct gttgaaaca ggaatggata gatgtaaaat taagatggaa
480

ccctgatgac tatggtgaa taaaagttt acgtgttct tcagactctt cgtggacacc
540

SequencesSSCPRe-file7August03.ST25.txt

agacatcatt ttgtttgata atgcagatgg acgtttgaa gggaccagta cgaaaacagt
600
catcaggtac aatggcactg tcacctggac tccaccggca aactacaaaa gttcctgtac
660
catagatgtc acgttttcc catttgacct tcagaactgt tccatgaaat ttggttcttg
720
gacttatgtat ggatcacagg ttgatataat tctagaggac caagatgttag acaagagaga
780
ttttttgtat aatggagaat gggagattgt gagtgcaaca gggagcaaag gaaacagaac
840
cgacagctgt tgctggtatac cgtatgtcac ttactcattt gtaatcaagc gcctgcctct
900
cttttatacc ttgttcctta taataccctg tattgggctc tcattttaa ctgtacttgt
960
cttctatctt cttcaaatg aaggtgaaaa gatttgtctc tgcacttcag tacttgtgtc
1020
tttgactgtc ttccttctgg ttattgaaga gatcatacca tcatttcaa aagtcatacc
1080
tctaattgga gagtatctgg tatattaccat gattttgtg acactgtcaa ttatggtaac
1140
cgcttcgct atcaacattc atcatcgta ttcctcaaca cataatgcc tggcgccctt
1200
ggtccgcaag atatttcttc acacgcttcc caaactgctt tcgatgagaa gtcatgtaga
1260
caggtacttc actcagaaag aggaaactga gagtggtagt ggaccaaaat cttctagaaaa
1320
cacattggaa gctgcgctcg attctattcg ctacattaca acacacatca tgaaggaaaa
1380
tgatgtccgt gaggttgttg aagattggaa attcatagcc caggttcttg atcggatgtt
1440
tctgtggact tttctttcg ttcaattgt tggatctttt gggcttttg ttccctgttat
1500
ttataaatgg gcaaataatata taataccagt tcatttggaa aatgcaaata agtgaaggcct
1560
cccaaggac tgaagtatac atttagttaa cacacatata tctgatggca cctataaaaat
1620

SequencesSSCPRe-file7August03.ST25.txt
tatgaaaatg taagttatgt gttaaattta gtgcaggctt taacagacta agttgctaa
1679

<210> 21
<211> 2664
<212> DNA
<213> Homo sapiens

<400> 21
gagagaacag cgtgaggcctg tggcttggtg tgctgagccc tcatacccttc ctggggccag
60

gctgggttt cacctgcaga atcgcttgg 120
120 ctggctgtcc tcagtgac

ctgcattgaag ccgttctggc tgccagagct ggacagcccc agaaaaaccc acctctctgc
180

agagcttgcc cagctgtccc cgggaaggcca aatgcctctc atgtaagtct tctgctcgac
240

ggggtgtctc ctaaacccctc actcttcagc ctctgtttga ccatgaaatg aagtgactga
300

gctctattct gtacctgcca ctctatttct ggggtgactt ttgtcagctg cccagaatct
360

ccaaggccagg ctgggtctct gcattccttc aatgacctgt tttttctgt aaccacaggt
420

tccgtggtga gaggaaggct cgcagaatcc agcagaatcc tcacagaatc cagcagcagc
480

tctgctgggg acatggtcca tggtgcaacc cacagcaaag ccctgacctg acctcctgtat
540

gctcaggaga agccatgggc ccctcctgtc ctgtgttctt gtccttcaca aagctcagcc
600

tgtgggtggct ctttctgacc ccagcagggtg gagagggaaatc taagcgccca cctcccgagg
660

ctcctggaga cccactctcc tctccctgtc ccacggcatt gcccggggaa ggctcgatata
720

ccgagactga ggaccggctc ttcaaacacc tcttccgggg ctacaaccgc tggcgcc
780

cgggtggccaa cacttcagac gtgggtgattt tgctgtttgg actgtccatc gctcagctca
840

tcgatgtggaa tgagaagaac caaatgtga ccaccaacgt ctggctaaaa caggagtgg
900

SequencesSSCPRe-file7August03.ST25.txt

gcgactacaa actgcgctgg aaccccaactg attttggcaa catcacatct ctcagggtcc
960

cttctgagat gatctggatc cccgacattg ttctctacaa caatgcagat ggggagtttg
1020

cagtgaccca catgaccaag gcccacctct tctccacggg cactgtgcac tgggtgcccc
1080

cggccatcta caagagctcc tgcagcatcg acgtcacctt ctcccccttc gaccagcaga
1140

actgcaagat gaagtttggc tcctggactt atgacaaggc caagatcgac ctggagcaga
1200

tggagcagac tgtggacctg aaggactact gggagagcgg cgagtgggcc atcgtcaatg
1260

ccacgggcac ctacaacagc aagaagtacg actgctgcgc cgagatctac cccgacgtca
1320

cctacgcctt cgtcatccgg cggctgccc tcttctacac catcaacctc atcatcccc
1380

gcctgctcat ctccctgcctc actgtgctgg tcttctacct gcctccgac tgccgcgaga
1440

agatcacgct gtgcatttcg gtgctgctgt cactcaccgt ctccctgctg ctcatcaactg
1500

agatcatccc gtccacacctg ctggtcatcc cgctcatcgg cgagtacctg ctgttcacca
1560

tgatcttcgt caccctgtcc atcgtcatca ccgtcttcgt gctcaatgtg caccacccgt
1620

cccccagcac ccacaccatg ccccactggg tgcggggggc ctttctgggc tgggtgcccc
1680

ggtggcttct gatgaaccgg cccccaccac ccgtggagct ctgccacccc ctacgcctga
1740

agctcagccc ctcttatcac tggctggaga gcaacgtgga tgccgaggag agggaggtgg
1800

tggtggagga ggaggacaga tggcatgtg caggtcatgt ggccccctct gtgggcaccc
1860

tctgcagcca cggccacctg cactctgggg ctcaggtcc caaggctgag gctctgctgc
1920

aggagggtga gctgctgcta tcacccaca tgcagaaggc actggaaggt gtgcactaca
1980

ttgccgacca cctgcggctc gaggatgctg actcttcggt gaaggaggac tggaaagtatg

2040

SequencesSSCPRe-file7August03.ST25.txt

ttgccatggc catcgacagg atcttcctct ggctgtttat catcgctgc ttccctgggg
2100

ccatcgccct ctttctgcct ccgttcctag ctggaaatgat ctgactgcac ctccctcgag
2160

ctggctccca gggcaaaggg gagggttctt ggatgtggaa gggctttgaa caatgtttag
2220

atttggagat gagcccaaag tgccagggag aacagccagg tgaggtggga ggttggagag
2280

ccaggtgagg tctctctaag tcaggctggg gttgaagttt ggagtctgac cgagtttgca
2340

gggtgctgag ctgtatggc cagcagggga gtaataaggg ctcttccgga aggggaggaa
2400

gcgggaggca ggcctgcacc tgatgtggag gtacaggcag atcttccta ccggggagg
2460

atggatggtt ggatacaggt ggctggcta ttccatccat ctggaaagcac atttggcct
2520

ccaggcttct ccttgacgac attcctctcc ttccctgctg caaaaatggct ctgcaccagc
2580

cggcccccaag gaggtctggc agagctgaga gccatggcct gcaggggctc catatgtccc
2640

tacgcgtgca gcaggcaaac aaga
2664

<210> 22

<211> 3020

<212> DNA

<213> Homo sapiens

<400> 22

gtcctccgc gggtccgagg gcgcgtggaaa cccagcggcg gcgaagcgga gaggagcccc
60

gcgcgtctcc gcccgcacgg ctccaggtct ggggtctgct ctggagccgc gcggggagag
120

gcgcgtctcg cgaccgcgc gcccgcctcc gaccgtccgg gtccgcggcc agcccgccca
180

ccagccatgg gctctggccc gctctcgctg cccctggcgc tgcgcgcgc gcccgtctg
240

ctgcgtctgc tgctgtctct gctgccagtg gccaggccct cagaggctga gcaccatcta

SequencesSSCPRe-file7August03.ST25.txt

300 tttgagccgc tgtttgaaga ttacaatgag atcatccggc ctgttagccaa cgtgtctgac
360 ccagtcatca tccatttcga ggtgtccatg tctcagctgg tgaagggtgga tgaagtaaac
420 cagatcatgg agaccaacct gtggctcaag caaatctgga atgactacaa gctgaagtgg
480 aaccctctg actatggtgg ggcagagttc atgcgtgtcc ctgcacagaa gatctggaag
540 ccagacattg tgctgtataa caatgctgtt ggggatttcc aggtggacga caagaccaa
600 gccttactca agtacactgg ggaggtgact tggatacctc cggccatctt taagagctcc
660 tgtaaaatcg acgtgaccta cttcccggtt gattacaaa actgtaccat gaagttcggt
720 tcctggtcct acgataaggc gaaaatcgat ctggcctga tcggctcttc catgaacctc
780 aaggactatt gggagagccg cgagtgggcc atcatcaaag ccccaggcta caaacacgac
840 atcaagtaca actgctgcga ggagatctac cccgacatca catactcgct gtacatccgg
900 cgccctgcct ttttctacac catcaacctc atcatccccct gcctgctcat ctcccttc
960 actgtgctcg ttttctacct gccctccgac tgcggtgaga aggtgaccct gtgcatttct
1020 gtcctccctc ccctgacggt gtttctcctg gtgatcactg agaccatccc ttccacctcg
1080 ctggcatcc ccctgattgg agagtacctc ctgttcacca tgattttgt aaccttgtcc
1140 atcgcatca ccgtcttcgt gctcaacgtg cactacagaa ccccggacac acacacaatg
1200 ccctcatggg tgaagactgt attcttgaac ctgctccccca gggtcatgtt catgaccagg
1260 ccaacaagca acgagggcaa cgctcagaag ccgaggcccc tctacggtgc cgagctctca
1320 aatctgaatt gtttcagccg cgcaagatcc aaaggctgca aggagggtcta ccctgccag
1380

SequencesSSCPRe-file7August03.ST25.txt

gacgggatgt gtggttactg ccaccaccgc aggataaaaa tctccaattt cagtgctaac
1440

ctcacgagaa gctctagttc tgaatctgtt gatgctgtgc tgtccctctc tgctttgtca
1500

ccagaaaatca aagaagccat ccaaagtgtc aagtatattt ctgaaaatat gaaagcacaa
1560

aatgaagcca aagagattca agatgattgg aagtatgttg ccatggtgat tgatcgatt
1620

tttctgtggg ttttcacctt ggtgtgcatt cttagggacag caggattgtt tctgcaaccc
1680

ctgatggcca gggaaagatgc ataagcacta agctgtgtgc ctgcctggga gacttccttg
1740

tgtcaggcga ggaggaggct gtttcctagt aagaacgtac tttctgttat caagctacca
1800

gctttgtttt tggcatttcg aggtttactt attttccact tatcttggaa tcatgaaaaa
1860

aaaaaaaaatgt caagagtatt tattaccat aaatgaacat ttaactagcc tttttggtat
1920

ggtaaagaga tgtcaaaatg tgattctatg tgatttagt gctatgctat ggaatataca
1980

tgtaaaaatg tttcctttt gttgttgaaa caaaaactggaa tagaaaaatg ctgttcagaa
2040

atatgaaaag tcattcagtt atcactacag atctcccagt aattttctt atttagcccc
2100

taatctcttt gaaggtttat actaattcag caatccccca tcgttaccca tttcttacca
2160

tgcatttctc gttcttact gggctaaag ggctatgcct ccatttcaga gagcttcaac
2220

tacttctctt gcatacttct aaattatact atgagaaaatc atgccttagtt attcattgtt
2280

aatataactg tcttagtaca ccataaaactg ggtggattat aaacaacaga aacttctcag
2340

tttggaggt tgggaggtcc aaggtcaagg caccagcaaa ttgggtgtct ggtgagggtc
2400

ctcttcctca aagggtgcct tctagctgtc tcctcacatg actgaaggga ctatgtatct
2460

SequencesSSCPRe-file7August03.ST25.txt

ctgtggggtc tatttataa gggcaactaac cccattcatg agacagagc cccatggcc
2520

taatcacctt tccaaggccc cacttctat ctaagacaat cacgctggga ataggttca
2580

acatatgaat tgggggagga cacatttggga ccacagcatg aacctttaga acagggttc
2640

tcagccttag cactacggac attttggct ggataaatat gtgttggtac agaatgggg
2700

tatccctgtgc attgttaggat cttagcagt accctagcct caactcacta gatgccaatg
2760

acataccttgc ttcttcacc agttatgata accaagaatg tctccattgt taaatgtccc
2820

cttaggagca aaattgcccc tggttgagaa acattgctt agacaaattt ttaagagttat
2880

catgtactac acttctgaaa cttAACGTGA tcATCACCAC tgACAGATGA ttCACAGAGA
2940

gagactgttt gaatcttgc tcactagttt ttccctgtca aaaataaaat ggacagaatt
3000

gcaaaaaaaaaaaaaaaa
3020

<210> 23

<211> 2664

<212> DNA

<213> Homo sapiens

<400> 23

gagagaacag cgtgagcctg tgtgcttgc tgctgagccc tcatccctc ctggggccag
60

gcttgggttt cacctgcaga atcgcttgc ctgggctgcc tgggctgtcc tcagtggcac
120

ctgcatgaag ccgttctggc tgccagagct ggacagcccc aggaaaaccc acctctctgc
180

agagcttgcc cagctgtccc cgggaagcca aatgcctctc atgtaagtct tctgctcgac
240

ggggtgtctc ctaaaccctc actcttcagc ctctgtttga ccatgaaatg aagtgactga
300

gctctattct gtacctgcca ctctatttct ggggtgactt ttgtcagctg cccagaatct
360

SequencesSSCPRe-file7August03.ST25.txt

ccaagccagg ctggttctct gcatttc aatgacgtt ttttttgtt aaccacagg
420

tccgtggta gaggaaggct cgcagaatcc agcagaatcc tcacagaatc cagcagc
480

tctgtgggg acatggtcca tggtgcaacc cacagcaaag ccctgacctg acctcctgat
540

gctcaggaga agccatgggc ccctcctgtc ctgtgttctt gtccttcaca aagctcagcc
600

tgtggtggtt ctttctgacc ccagcagggtg gagaggaagc taagcgccc cctcccagg
660

ctcctggaga cccactctcc tctcccagtc ccacggcatt gccgcaggga ggctcgata
720

ccgagactga ggaccggctc ttcaaaccacc tcttccgggg ctacaaccgc tggcgcgcc
780

cgggtccccaa cacttcagac gtggtgattt tgctgtttgg actgtccatc gctcagctca
840

tcgatgtgga tgagaagaac caaatgatga ccaccaacgt ctggctaaaa caggagtgg
900

gcgattacaa actgcgctgg aaccccgctg atttggcaa catcacatct ctcagggtcc
960

cttctgagat gatctggatc cccgacattt ttctctacaa caatgcagat ggggagttt
1020

cagtgaccca catgaccaag gcccacctct tctccacggg cactgtgcac tgggtgcccc
1080

cggccatcta caagagctcc tgcagcatcg acgtcacctt cttcccttc gaccagcaga
1140

actgcaagat gaagtttggc tcctggactt atgacaaggc caagatcgac ctggagcaga
1200

tggagcagac tgtggacctg aaggactact gggagagcgg cgagtgggcc atcgtaatg
1260

ccacgggcac ctacaacagc aagaagtacg actgctgcgc cgagatctac cccgacgtca
1320

cctacgcctt cgtcatccgg cggctgccgc tcttctacac catcaacctc atcatccc
1380

gcctgctcat ctccctgcctc actgtgctgg tcttctacat gcccctccgac tggggcgaga
1440

agatcacgct gtgcatttcg gtgctgctgt cactcaccgt ctccctgctg ctcatcactg

1500

SequencesSSCPRe-file7August03.ST25.txt

agatcatccc gtccacactcg ctggtcatcc cgctcatcg cgagtacctg ctgttaccca
1560

tgatcttcgt caccctgtcc atcgtcatca ccgtcttcgt gctcaatgtg caccaccgct
1620

cccccagcac ccacaccatg ccccactggg tgcggggggc cttctgggc tgtgtgcccc
1680

ggtggtttct gatgaaccgg cccccaccac ccgtggagct ctgccacccc ctacgcctga
1740

agtcagccc ctcttatcac tggctggaga gcaacgtgga tgccgaggag agggaggtgg
1800

tggtgagga ggaggacaga tggcatgtg caggtcatgt ggccccctct gtgggcaccc
1860

tctgcagcca cggccacactg cactctgggg ctcaggatcc caaggctgag gctctgctgc
1920

aggagggtga gctgctgcta tcacccaca tgcagaaggc actgaaagggt gtgcactaca
1980

ttgccgacca cctgcggct gaggatgctg actcttcgtt gaaggaggac tggaaagtatg
2040

ttgccatggc catcgacagg atcttcctct ggctgtttat catgtctgc ttccctgggg
2100

ccatcgccct cttctgcct ccgttccttag ctggaatgtat ctgactgcac ctccctcgag
2160

ctggctccca gggcaaaggg gagggttctt ggatgtggaa gggctttgaa caatgttttag
2220

attggagat gagccaaag tgccagggag aacagccagg tgaggtggaa ggttggagag
2280

ccaggtgagg tctctctaag tcaggctggg gttgaagttt ggagtctgtc cgagtttgca
2340

gggtgctgag ctgtatggtc cagcagggga gtaataaggg ctcttcggg aggaggaggg
2400

gcgggaggca ggcctgcacc tgatgtggag gtacaggcag atcttccta ccggggagg
2460

atggatggtt ggatacaggt ggctggcta ttccatccat ctggaaagcac atttgaccc
2520

ccaggcttct cttgacgat attcctctcc ttcccttgctg caaaatggct ctgcaccage
2580

SequencesSSCPRe-file7August03.ST25.txt

cgccccccag gaggtctggc agagctgaga gccatggcct gcaggggctc catatgtccc
2640

tacgcgtgca gcaggcaaac aaga
2664

<210> 24
<211> 2664
<212> DNA
<213> Homo sapiens

<400> 24
gagagaacag cgtgagcctg tgtgcttgg tgctgagccc tcatcccctc ctggggccag
60

gcttgggttt cacctgcaga atcgcttgg tgggctgcc tgggctgtcc tcagtggcac
120

ctgcatgaag ccgttctggc tgccagagct ggacagcccc aggaaaaccc acctctctgc
180

agagcttgcc cagctgtccc cgggaagcca aatgcctctc atgtaagtct tctgctcgac
240

ggggtgtctc ctaaacccctc actcttcagc ctctgtttga ccatgaaatg aagtgactga
300

gctctattct gtacctgcca ctctatttct ggggtgactt ttgtcagctg cccagaatct
360

ccaagccagg ctggttctct gcattccttc aatgacctgt tttcttctgt aaccacaggt
420

tcggtgtga gaggaagcct cgccagaatcc agcagaatcc tcacagaatc cagcagcagc
480

tctgctgggg acatggtcca tggtgcaacc cacagcaaag ccctgacctg acctcctgat
540

gctcaggaga agccatgggc ccctcctgtc ctgtgttctt gtccttcaca aagtcagcc
600

tgttgtggct cttctgacc ccagcaggtg gagaggaagc taagcgccca cttcccgagg
660

ctcctggaga cccactctcc tctccctgtc ccacggcatt gcccgcaggga ggctcgata
720

ccgagactga ggaccggctc ttcaaacacc tcttccgggg ctacaaccgc tggcgcc
780

cggtgcccaa cacttcagac gtgggtgattt tgctgtttgg actgtccatc gctcagctca
840

SequencesSSCPRe-file7August03.ST25.txt

ccagccatgg gctctggccc gctctcgctg cccctggcgc tgtcgcgcgc gcccgtgctg
240

ctgctgctgc tgctgtctct gctgccagtg gccagggcct cagaggctga gcaccgtcta
300

tttgagcggc tggtaaga ttacaatgag atcatccggc ctgtggccaa cgtgtctgac
360

ccagtcatca tccatttcga ggtgtccatg tctcagctgg tgaagggtgga tgaagtaaac
420

cagatcatgg agaccaacct gtggctcaag caaatctgga atgactacaa gctgaagtgg
480

aaccctctg actatggtgg ggcagagttc atgcgtgtcc ctgcacagaa gatctggaag
540

ccagacattt tgctgtataa caatgctgtt gggatttcc aggtggacga caagaccaaa
600

gccttactca agtacactgg ggaggtgact tggataacctc cggccatctt taagagctcc
660

tgtaaaatcg acgtgaccta cttcccggtt gattacaaa actgtaccat gaagttcggt
720

tcctggtcct acgataaggc gaaaatcgat ctggcctga tcggctcttc catgaacctc
780

aaggactatt gggagagcgg cgagtgggcc atcatcaaag ccccaggcta caaacacgac
840

atcaagtaca actgctgcga .ggagatctac cccgacatca catactcgct gtacatccgg
900

cgccctccct tggtaacac catcaacctc atcatccctt gcctgctcat ctcccttc
960

actgtgctcg tcttctaccc gccctccgac tgccgtgaga aggtgaccct gtgcatttct
1020

gtcctccctt ccctgacggt gtttcctgt gtgatcactg agaccatccc ttccaccccg
1080

ctggtcatcc ccctgattgg agagtacctc ctgttacca tgattttgt aaccttgc
1140

atcgcatca ccgtcttcgt gtcacgtg cactacagaa ccccggacacacacaatg
1200

ccctcatggg tgaagactgt attcttgaac ctgctcccc gggtcatgtt catgaccagg
1260

ccaacaagca acgaggcggc cgtcagaag ccgaggcccc tctacggtgc cgagctctca

1320

SequencesSSCPRe-file7August03.ST25.txt

aatctgaatt gcttcagccg cgcaagagtcc aaaggctgca aggagggcta cccctgccag
1380
gacgggatgt gtggttactg ccaccaccgc aggataaaaaa tctccaattt cagtgctaac
1440
ctcacgagaa gctctagttc tgaatctgtt gatgctgtgc tgtccctctc tgctttgtca
1500
ccagaaaatca aagaagccat ccaaagtgtc aagtatattt ctgaaaatat gaaagcacaa
1560
aatgaagcca aagagattca agatgattgg aagtatgttgc ccatggtgat tgatcgatt
1620
tttctgtggg ttttcaccct ggtgtgcatt ctagggacag caggattgtt tctgcaaccc
1680
ctgatggcca gggaaagatgc ataagcacta agctgtgtgc ctgcctggga gacttccttg
1740
tgtcaggcga ggaggaggct gcttcctagt aagaacgtac tttctgttat caagctacca
1800
gctttgttt tggcatttcg aggtttactt attttccact tatcttgaa tcatgcaaaaa
1860
aaaaaaaaatgt caagagtatt tattaccgtt aaatgaacat ttaactagcc tttttggat
1920
ggtaaagaga tgtcaaaatg tgattctatg tgatttagtat gctatgctat ggaatataca
1980
tgtaaaaatg ttccctttt gttgttggaa caaaactggaa tagaaaaatg ctgttcagaa
2040
atatgaaaag tcattcagtt atcactacag atctcccagt aattttctt atttagccca
2100
taatctcttt gaaggtttat actaattcag caatccccca tcgttaccca tttcttacca
2160
tgcatcttc gttcttact-gggtctaaag ggctatgcct ccatttcaga gagctcaac
2220
tacctctctt gcataacttctt aaattatact atgagaaatc atgcctagtt attcattgtt
2280
aatataactg tcttagtaca ccataaaactg ggtggattat aaacaacaga aacttctcag
2340
tttggaggt tgggaggtcc aaggtaagg caccagcaaa tttgggtctt ggtgagggtc
2400

SequencesSSCPRe-file7August03.ST25.txt

ctcttcctca aagggtgcct tctagctgtg tcctcacatg actgaaggga ctatct
2460

ctgtgggtc tatttataa gggactaac cccattcatg agagcagagc cccatggcc
2520

taatcacctt tccaaggccc cacattctat ctaagacaat cacgctggga ataggttca
2580

acatatgaat tgggggagga cacatttggaa ccacagcatg aacctttaga acagggtttc
2640

tcagccttag cactacggac attttggct ggataaatat gtgttggtac agaatgggg
2700

tatcctgtgc attgtaggat cttagcagt accctagcct caactcacta gatgccaatg
2760

acataccttgc ttcttcacc agttatgata accaagaatg tctccattgt taaatgtccc
2820

cttaggagca aaattgcccc tggttgagaa acattgctt agacaaattt ttaagagttat
2880

catgtactac acttctgaaa cttaacgtga tcatcaccac tgacagatga ttcacagaga
2940

gagactgttt gaatcttgc tcaactgttt ttcctgtca aaaataaaat ggacagaatt
3000

gaaaaaaaaaaaaaaa
3020

<210> 26

<211> 3020

<212> DNA

<213> Homo sapiens

<400> 26

gtcctccgc gggtccgagg gcgctggaaa cccagcggcg gcgaagcggaa gaggagcccc
60

gccccgtctcc gccccacgg ctccaggctt ggggtctgcg ctggagccgc gccccggagag
120

gccgtctctg cgaccgcccgc gccccgtccc gaccgtccgg gtccgcggcc agccccggcca
180

ccagccatgg gctctggccc gctctcgctg cccctggcg tcgtcgccgc gcccgtctg
240

ctgctgtgc tgctgtctt gctgccagt gccagggcct cagaggtga gcaccgtcta
300

SequencesSSCPRe-file7August03.ST25.txt

tttgagcggc tgttgaaga ttacaatgag atcatccgc ctgttagccaa cgtgtctgac
360
ccagtcatca tccatttcga ggtgtccatg tctcagctgg tgaagggtgga tgaagtaaac
420
cagatcatgg agaccaacct gtggctcaag caaatctgga atgactacaa gctgaaatgg
480
aaccctctg actatggtgg ggcagagttc atgcgtgtcc ctgcacagaa gatctggaag
540
ccagacattg tgctgtataa caatgctgtt ggggatttcc aggtggacga caagaccaa
600
gccttactca agtacactgg ggaggtgact tggatacctc cggccatctt taagagctcc
660
tgtaaaatcg acgtgaccta cttcccggtt gattacaaa actgtaccat gaagttcggt
720
tcctggtcct acgataaggc gaaaatcgat ctggtcctga tcggctcttc catgaacctc
780
aaggactatt gggagagcgg cgagtggcc atcatcaaag ccccaggcta caaacacgac
840
atcaagtaca actgctgcga ggagatctac cccgacatca catactcgct gtacatccgg
900
cgctgcccct tgttctacac catcaacctc atcatcccct gcctgctcat ctcccttcctc
960
actgtgctcg tcttctacct gccctccgac tgcggtgaga aggtgaccct gtgcatttct
1020
gtcctccctc ccctgacggt gtttctcctg gtgatcactg agaccatccc ttccacctcg
1080
ctggtcatcc ccctgattgg agagtacctc ctgttcacca tgattttgt aaccttgtcc
1140
atcgcatca ccgttccgt gctcaacgtg cactacagaa ccccgacgac acacacaatg
1200
ccctcatggg tgaagactgt attcttgaac ctgctcccc gggcatgtt catgaccagg
1260
ccaacaagca acgagggcaa cgctcagaag ccgaggcccc tctacggtgc cgagctctca
1320
aatctgaatt gcttcagccg cgcagagtcc aaaggctgca aggagggcta cccctgccag
1380

SequencesSSCPRe-file7August03.ST25.txt

gacgggatgt gtggtaactg ccaccaccgc aggataaaaa tctccaattt cagtgcataac
1440

ctcacgagaa gctctagttc tgaatctgtt gatgctgtgc tgtccctctc tgctttgtca
1500

ccagaaaatca aagaagccat ccaaagtgtc aagtatattg ctgaaaatat gaaagcacaa
1560

aatgaagcca aagagattca agatgattgg aagtatgttg ccatggtgat tgatcgatt
1620

tttctgtggg ttttcaccct ggtgtgcatt ctagggacag caggattgtt tctgcaaccc
1680

ctgatggcca gggaaagatgc ataagcacta agctgtgtgc ctgcctggga gacttccttg
1740

tgcaggcga ggaggaggct gtttcctagt aagaacgtac tttctgttat caagctacca
1800

gctttgtttt tggcatttcg aggtttactt atttccact tatcttgaa tcatgcaaaa
1860

aaaaaaaaatgt caagagtatt tattaccgtt aaatgaacat ttaactagcc tttttggat
1920

ggtaaaagaga tgtcaaaatg tgattctatg tgatttagt gctatgtat ggaatataca
1980

tgtaaaaatg tttccttttta gttgttgaaa caaaactgga tagaaaaatg ctgttcagaa
2040

atatgaaaag tcattcagtt atcactacag atctcccagt aatttttctt atttagcccc
2100

taatctctt gaaggtttat actaattcag caatccccca tcgttaccca tttcttacca
2160

tgcatttctc gttcttact gggctaaag ggctatgcct ccatttcaga gagcttcaac
2220

tacttctctt gcataacttct aaattataact atgagaaaatc atgccttagtt attcattgtt
2280

aatataactg tcttagtaca ccataaaactg ggtggattat aaacaacaga aacttctcag
2340

tttggaggt tgggaggtcc aaggtaagg caccagcaaa tttgggtct ggtgagggtc
2400

ctcttcctca aagggtgcct tctagctgtc tccctcacatg actgaaggga ctagctatct
2460

ctgtggggtc tattttataa gggcactaac cccattcatg agagcagagc ccccatggcc

2520

SequencesSSCPRe-file7August03.ST25.txt

taatcacctt tccaaggccc caccttctat ctaagacaat cacgctggga ataggttca
2580

acatatgaat tgggggagga cacatttggga ccacagcatg aacctttaga acagggtttc
2640

tcagccttag cactacggac attttgggct ggataaatat gtgttggtac agaatgggg
2700

tatcctgtgc attgttaggat cttagcagt accctagcct caactcacta gatgccaatg
2760

acataccttgc ttcttcacc agttatgata accaagaatg tctccattgt taaatgtccc
2820

cttaggagca aaattgcccc tggttgagaa acattgcttt agacaaattt ttaagagtat
2880

catgtactac acttctgaaa cttAACGTGA tcATCACCAC tgACAGATGA tTCACAGAGA
2940

gagactgttt gaatcttgc tcactagttt ttccctgtgc aaaataaaat ggacagaatt
3000

gcaaaaaaaaaaaaa
3020

<210> 27
<211> 3020
<212> DNA
<213> Homo sapiens

<400> 27
gtccctccgc gggtccgagg gcgctggaaa cccagcggcg gcgaagcggga gaggagcccc
60

gccccgtctcc gcccccacgg ctccaggctc ggggtctgcg ctggagccgc gccccggagag
120

gccccgtctcg cgaccgcccgc gccccgtccc gaccgtccgg gtccgcggcc agccccggcca
180

ccagccatgg gctctggccc gctctcgctg cccctggcgcc tgtcgcgc gcccgtctcg
240

ctgctgtgc tgctgtctct gctgccagtg gccagggcct cagaggctga gcaccgtcta
300

ttttagccgc tgtttgaaga ttacaatgag atcatccggc ctgttagccaa cgtgtctgac
360

ccagtcata tccatttcga ggtgtccatg tctcagctgg tgaagggtgga tgaagtaaac

420

SequencesSSCPRe-file7August03.ST25.txt

cagatcatgg agaccaacct gtggctcaag caaatctgga atgactacaa gctgaagtgg
480
aacccctctg actatggtgg ggcagagttc atgcgtgtcc ctgcacagaa aatctggaag
540
ccagacattg tgctgtataa caatgctgtt ggggatttcc aggtggacga caagacaaa
600
gccttaactca agtacactgg ggaggtgact tggatacctc cggccatctt taagagctcc
660
tgtaaaatcg acgtgaccta cttcccggtt gattacaaa actgtaccat gaagttcggt
720
tcctggtcct acgataaggc gaaaaatcgat ctggcctga tcggcttcc catgaacctc
780
aaggactatt gggagagcgg cgagtgggcc atcatcaaag ccccaggcta caaacacgac
840
atcaagtaca actgctgcga ggagatctac cccgacatca catactcgct gtacatccgg
900
cgccctgcct tgttctacac catcaacctc atcatccct gcctgctcat ctcccttcctc
960
actgtgctcg tcttctacct gccctccgac tgcggtgaga aggtgaccct gtgcatttct
1020
gtcctcctct ccctgacggt gtttctcctg gtgatcactg agaccatccc ttccacctcg
1080
ctggtcatcc ccctgattgg agagtacctc ctgttcacca tgatTTTGT aaccttgc
1140
atcgcatca ccgtcttcgt gctcaacgtg cactacagaa ccccgacgac acacacaatg
1200
ccctcatggg tgaagactgt attcttgaac ctgtccccca gggtcatgtt catgaccagg
1260
ccaacaagca acgaggggcaa cgctcagaag ccgaggcccc tctacggtgc cgagctctca
1320
aatctgaatt gtttcagccg cgcagagtcc aaaggctgca aggagggcta cccctgcccag
1380
gacgggatgt gtggttactg ccaccaccgc aggataaaaaa tctccaattt cagtgctaac
1440
ctcacgagaa gctcttagttc tgaatctgtt gatgctgtgc tgcccttc tgctttgtca
1500

SequencesSSCPRe-file7August03.ST25.txt

ccagaaatca aagaagccat ccaaagtgc aagtatattg ctgaaaatat gaaaggcaca
1560
aatgaagcca aagagattca agatgattgg aagtatgttg ccatggtgat tgatcgatt
1620
tttctgtggg tttcacccct ggtgtgcatt ctagggacag caggattgtt tctgcaaccc
1680
ctgatggcca gggaaagatgc ataagcacta agctgtgtgc ctgcctggga gacttccttg
1740
tgccaggca ggaggaggct gtttcctagt aagaacgtac tttctgttat caagctacca
1800
gctttgttt tggcatttcg aggtttactt atttccact tatcttgaa tcatgcaaaa
1860
aaaaaaaaatgt caagagtatt tattaccgt aaatgaacat ttaactagcc tttttggat
1920
ggtaaagaga tgtcaaaatg tgattctatg tgatttagtat gctatgttat ggaatataca
1980
tgtaaaaatg ttcccttta gttgttggaa caaaactgga tagaaaaatg ctgttcagaa
2040
atatgaaaag tcattcagtt atcactacag atctcccagt aattttctt atttagccca
2100
taatctctt gaaggtttat actaattcag caatccccca tcgttacccca tttcttacca
2160
tgcatttctc gttcttact gggctaaag ggctatgcct ccatttcaga gagttcaac
2220
tacttctctt gcataacttct aaattatact atgagaaatc atgccttagtt attcattgtt
2280
aatataactg tcttagtaca ccataaaactg ggtggattat aaacaacaga aacttctcag
2340
tttggaggt tgggaggtcc aaggtcaagg caccagcaaa tttggtgtct ggtgagggtc
2400
ctcttcctca aagggtgcct tctagctgtc tcctcacatg actgaaggga ctatgttatct
2460
ctgtgggtc tattttataa gggactaac cccattcatg agagcagagc ccccatggcc
2520
taatcacctt tccaaggccc caccttctat ctaagacaat cacgctggga ataggttca
2580

SequencesSSCPRe-file7August03.ST25.txt
acatatgaat tgggggagga cacatttggaa ccacagcatg aacctttaga acagggtttc
2640
tcagccttag cactacggac attttgggct ggataaatat gtgttgtac agaatggggg
2700
tatccctgtgc attgttaggat cttagcagt acccttagcct caactcacta gatgccaatg
2760
acatacaccc ttttttacc accatgtata accaagaatg tctccattgt taaatgtccc
2820
cttaggagca aaattgcccc tggttgagaa acattgctt agacaaattt ttaagagtat
2880
catgtactac acttctgaaa cttAACGTGA tcattaccac tgacagatga ttcacagaga
2940
gagactgttt gaatcttgc tcactagttt ttccctgtca aaaataaaat ggacagaatt
3000
gcaaaaaaaaaaaaaaaa
3020

<210> 28
<211> 210
<212> DNA
<213> Homo sapiens

<400> 28
ggctgtttt gccaattctt gggcatcccc ggggtgtgt agctttgccc taggctgttc
60

ccttggaaagcg aggttgacac aacttcttcc ccacacacag gagtggagcg actacaaact
120

gcgttggaaac cccgttgatt ttggcaacat cacatcttc agggccctt ctgagatgt
180

ctggatcccc gacattgttc tctacaacaa
210

<210> 29
<211> 210
<212> DNA
<213> Homo sapiens

<400> 29
agcagggttg gggagtcacc aagatgggtg gtgccacggg aagtaaaacc aggctgattc
60

ttttaccgtc tcccttctccc tccctgtttc cttcccccag atctggaatg actacaagct
120

SequencesSSCPRe-file7August03.ST25.txt

gaagtggAAC ccctctgact atgggtgggc agagttcatg cgtgtccctg cacagaagat
180

ctggaagCCA gacattgtgc tgtataacaa
210

<210> 30

<211> 210

<212> DNA

<213> Homo sapiens

<400> 30

atctggaatg actacaagct gaagtggAAC ccctctgact atgggtgggc agagttcatg
60

cgtgtccctg cacagaagat ctggaagCCA gacattgtgc tgtataacaa gtaaggcct
120

ggggggccca cgccctctca gggctgtcag cctgggctct gggttttgg cccactgtgc
180

ttaaaacctg gccttccttg gcctttcca
210

<210> 31

<211> 7438

<212> DNA

<213> Homo sapiens

<400> 31

gctgagcctg agcccgaccc gggcgccctc ccggcaggca ccatggtgca gaagtcgcgc
60

aacggcgccg tataccccgg cccgagcggg gagaagaagc tgaaggtggg cttcgtggg
120

ctggaccctcg ggcgcggccga ctccacccgg gacggggcgc tgctgatcgc cggctccgag
180

gcccccAAC gcggcagcat cctcagcaa cctcgccgg gcggcgccgg cccgggaag
240

cccccccaag cgcaacgcct tctaccgcaa gctcagaat ttccctctaca acgtgctgga
300

gcggccgcgc ggctgggcgt tcataccatca cgcctacgtg ttccctctgg ttttctcctg
360

cctcgtgctg tctgtgtttt ccaccatcaa ggagtatgag aagagctcgg agggggccct
420

ctacatcctg gaaatcgtga ctatcgtggt gtttggcgtg gagtacttcg tgccggatctg

SequencesSSCPRe-file7August03.ST25.txt

480

ggccgcaggc tgctgctgcc ggtaccgtgg ctggaggggg cggctcaagt ttgcccggaa
540

accgttctgt gtgattgaca tcatggtgct catcgctcc attgcggtgtc tggccgcccgg
600

ctccccagggc aacgtctttg ccacatctgc gctccggagc ctgcgccttc tgcatgattct
660

gcggatgatc cgcatggacc ggccggggagg cacctggaag ctgctggct ctgtggtcta
720

tgcggcacagc aaggagctgg tcactgcctg gtacatcgcc ttcccttgtc tcatcctggc
780

ctcggttcctg gtgtacttgg cagagaaggg ggagaacgac cactttgaca cctacgcggaa
840

tgcactctgg tggggcctga tcacgctgac caccattggc tacggggaca agtaccccca
900

gacctggaac ggcaggctcc ttgcggcaac cttcacccctc atcgggtgtct ccttcttcgc
960

gctgcctgca ggcacatttgg ggtctgggtt tgccctgaag gttcaggagc agcacaggca
1020

gaagcacttt gagaagaggc ggaacccggc agcaggcctg atccagtcgg cctggagatt
1080

ctacgccacc aacctctcgc gcacagacccct gcactccacg tggcagtact acgagcgaac
1140

ggtcaccgtg cccatgtaca gttcgcaaac tcaaacctac ggggcctcca gacttatccc
1200

cccgctgaac cagctggagc tgctgaggaa cctcaagagt aaatctggac tcgctttcag
1260

gaaggacccc ccgccccggc cgtctccaag ccagaaggc agtttggaaag atcgtgtctt
1320

ctccagcccc cgaggcgtgg ctgccaaggga gaaggggtcc ccgcaggccc agactgtgag
1380

gcggtcaccc agcgccgacc agagcctcga ggacagcccc agcaagggtgc ccaagagctg
1440

gagcttcggg gaccgcagcc gggcacgcca ggcttccgc atcaagggtg ccgcgtcact
1500

gcagaactca gaagaagcaa gcctccccgg agaggacatt gtggatgaca agagctgccc
1560

SequencesSSCPRe-file7August03.ST25.txt

ctgcgagttt gtgaccgagg acctgacccc gggcctcaaa gtcagcatca gagccgtgt
1620

tgtcatgcgg ttcctggtgt ccaagcgaa gttcaaggag agcctgcggc cctacgacgt
1680

gatggacgtc atcgagcagt actcagccgg ccacctggac atgctgtccc gaattaagag
1740

cctgcagtcc agagtggacc agatcgtggg gcggggccca gcgatcacgg acaaggaccg
1800

caccaagggc ccggccgagg cgagactgcc cgaggacccc agcatgatgg gacggctcgg
1860

gaaggtggag aagcaggtct tgtccatgga gaagaagctg gacttcctgg tgaatatcta
1920

catgcagcgg atgggcatcc ccccgacaga gaccgaggcc tactttgggg ccaaagagcc
1980

ggagccggcg ccgcccgtacc acagccccga agacagccgg gagcatgtcg acaggcacgg
2040

ctgcattgtc aagatcgtgc gtcgcagcag ctccacggc cagaagaact tctcggcgcc
2100

cccgccggcg cccctgtcc agtgtccggc ctccacctcc tggcagccac agagccaccc
2160

gcgccaggc cacggcacct cccctgtggg ggaccacggc tccctggtgc gcatccgccc
2220

gccgcctgcc cacgagcggt cgctgtccgc ctacggcggg ggcaaccggcg ccagcatgga
2280

gttcctgcgg caggaggaca ccccggtcg caggccccc gaggggaccc tgccggacag
2340

cgacacgtcc atctccatcc cgtccgtgga ccacgaggag ctggagcggt cttcagcgg
2400

cttcagcatc tcccagtcca aggagaacct ggatgtctc aacagctgct acggcccggt
2460

gggcgccttgt gccaaagtca ggccctacat tgcggaggaa gagtcagaca ccgactccga
2520

cctctgtacc ccgtgcgggc ccccgccacg ctggccacc ggcgagggtc ctttggta
2580

cgtgggctgg gcccggccca ggaagtgagg cggcgctggg ccagtggacc cgcccgccggc
2640

SequencesSSCPre-file7August03.ST25.txt
cctcctcagc acgggcgc cgggttttgg aggccggaaac cctctggggc ccttttctta
2700
cagtaactga gtgtggcgaaa aagggtgggc cctggagggg cccatgtggg ctgaaggatg
2760
ggggctcctg gcagtgaccc tttacaaaag ttatcccacca acaggccact cccaggccct
2820
gtcgccattg aggtgcctcc gctggctgt ctccctcaccc ctccctgtgc tggagcctgt
2880
ccccaaaaagg tgccaactgg gaggcctcgg aagccactgt ccaggctccc actgcctgtc
2940
tgctctgttc ccaaaggcag cgtgtgtggc ctggggccct gcggtggcat gaagcatccc
3000
ttctgggtgtg ggcatacgcta cgtgtttgg gggcagcggtt tcacggcggt gcccttgctg
3060
tctcccttgg gctggctcga gcctggggc catgtccctt tgccgtcccc tcatggggca
3120
ggaaatccat agcggggccc acaggcaggg gtatgagtgc gtcccaccca acgcagcacc
3180
agccccggcc accgctcccc gtgtccccag ttccgtctca getacctggc ctccaggacc
3240
ctggagaagg gagacctggc agtggaggga ggctgtgctg tgtgtcccc tgcaggtgtg
3300
accggcctg ctctttctc cccggcagg tgtggccccg cctgctctt cctccccac
3360
cagtatggcc ccacctgctc tttcctcccc cccaaagggtg tggccccacc ttttcttcc
3420
tccctgtcccg aggtgtgacc ccacctgctc tttcctccct cccagtatgg ccccacctgc
3480
tcttcctcc cccgaggtga ggccccgcct gctcttcct cccatggag ccgctgaggc
3540
gtgcgcaccc gggcacaggt tggggctctg caggatgagg aagacaggcc aatcccttcc
3600
ctcccagaag ctggccgccc agcaggaggg actgaggcca gactcatgtc cagcaaggaa
3660
cgtgtgggtgt gtccctggg aagtctctgg gcccctggaa gagggaaaggt gcacgtcctg
3720
ggatgggtgc gggccctgt tttggagac aaagggtag agggtctgtc ttggggcccc

3780

SequencesSSCPRe-file7August03.ST25.txt

ccagactcta gcccggcag tgcagccacc tactgcccc cctcagagaa gtgcagcg 3840
aaggaggctg gaggtggtgc ggcgctgcct cgggtgtctg cgtaatgag cgtggccaag 3900
gaccagtgcc acctcatggc aaagagctcc cgcaatgttt gtttagagtgc acatcctacg 3960
tgcccactgg cacacacacg tgctcacata catgtcccg tacaggcgta cacatgcacg 4020
cttgcacaca tgcacacaga ccacatagca cacatgtgca ctgaccacac ctgtatagac 4080
catgcacagt acacatacgt gcatacacat gcctgcatac aggatacac atgcacgctt 4140
acatgtacac gtgcacagat cacacacatg cacacacgtg tagtcacac acagtataca 4200
catacacaag tgcacagacc acacacagca ctaacacatg cacacacaaa gtgcataaggc 4260
cacacagcac atgcacacacg gtgcacagac cacacagcac acacaagtgc acagagcaca 4320
ctgcacacat gcacacacac acgcgtgcat gcacactcct cgcaacttcca gccttggagc 4380
ccttctgtct ctggctttc tcttgaccc tgctgagtgt aagctgcctg gggaggggct 4440
acaaggagta attgtggctt taggggtcgt ggtgatgctg gaatgtcaag cggcgctgt 4500
gggtatccga ctgtccgggc tcctggtccg cagtggcaga ggcgcaggca gagccaatca 4560
gggtctcgtg ctgccttcc cccccacagc ctggcagcca tccagaggag gggctctacc 4620
agatgccaag gtgccccggt gtctgtatgg gtgtccgggtt gggctctgtg tttggtctgc 4680
cctggaggtg gctggccct cctggatgg gtggctcagc ctcgaatccc aggccccagc 4740
ccaggcaggt gctgctgcct gttgtggttt cctggccag cttcttc tccctctgca 4800
taaaaatcaca gtccgtgagt cttccagctg ccaccacggc tgggacacgc tgggggaggg 4860

SequencesSSCPRe-file7August03.ST25.txt

ctcctccat gcctcctgca cacagccgtc tgagcagggc aggtgccaaac accccccacc
4920
ggagacacgc tgcccctcag cgatgcccct acctttggg gggcctcgtc tcaagcccc
4980
ccttggaggg tgaaatcacc ccaggcactg tgagggcttc tccagggggga caccctttga
5040
gctgtgggtc tgatcacccc aagtcccgca cacggaggag aggcacagcc agggcgtgtg
5100
gttaatgtt tgccccttcg gggctggagg tctcagtgtt tctagattcc agaccctgct
5160
gccagagaga cctgctgccc gagagaaggg gaggaggact ccagctggc tcggcccccc
5220
acagtcaggg acccccataa aggacacccc cttctctcta gaaagagctg ggctctcagc
5280
tatttctagt tgcttcccag aagccgagga gcagaaggag ctgtgagagc ttgcagaaa
5340
cccccttgc cccgcctcc tgagctatga atgccgtaca gagcagaggc tggggcattg
5400
gcaagatcac aggttgatgc tgcacagccc cattgacaca aaccctcaaa gcagacgtga
5460
gagggacggc tcacaaagct tggacctgcc gtggagggtg cccggcagac gtggcgtgag
5520
aggacggct cacgaggctt ggacctgctg tggagggtgcc ccagcagacg tggtgtgaga
5580
ggaacggctc acgagacttg gacctggtgg agggtgccca gcagacgtgg tgtgagaggg
5640
acggctcaca gggcttggac cggagagaga tggctcatga gacttggacc tgccgtggag
5700
ggtgcccagc agacgtggta tgagagggat ggctcacgag gcttggacct ggtggaggg
5760
ccccggcaga cgtgtgagag ggacggttca caaggcttgg acctgccatg gagggtgccc
5820
agcagacgtg gtgtgagagg gacagctcac gaggcttggc cctgcccgtgg agggtgccca
5880
gcagggggct gagctcttag gggtggtgc tcagtgcacg ggtgccccca gtgtcctctg
5940

SequencesSSCPRe-file7August03.ST25.txt
atccctgtccg gtgcctcccc caaccccccac acccatgcag aactcccaagg tcacatgcac
6000
gtatgtccag ggcatttttttggcgtgaag aggccctggtc agggccttta ggggctgcag
6060
gacggaatgg ccacccctgggg agcctgtgtg gctgtgccgg gcagccatcc tgcattccca
6120
cccagcgccgc agtctccacc tcggcccccag caaagcgcta agcagccgga gagacagcca
6180
ggcgcccttc ctgaaggatg tggatggtg gactccgggg tcgagggaaat acgcagggttc
6240
ctgtcctccg ggagacctag agaagctgca caccaggag ctttccatga cccgggagca
6300
tgagtgaatg gggggttcca gtttgctgaa ctttgctgtc ttgttaagggt gggggctgac
6360
ggccgaccct gggaggaggt gacaccgcag ggggagggttgg tggcaacgg tggaggagga
6420
gagacgggag gggaccattt gggatggagg ggcctttca gagttttaaa aggctttgt
6480
ggggtgtggagt tgagtgtgtcttgg acacttgccg tggtgccctt ggctggccga
6540
ggagactggc tctggccagg gccccgtctt gagaggtctt cagcgtctga ctctcgccca
6600
ggcccccagca aggaggggccc ggtccccggg gctaccaggc aggcacgtgc acatcgccat
6660
cgccacacgc caactccgc tgggttttac aaagtgcgttgc ccttaatgca tgtggacagg
6720
aactccctga ggtcgccccca tgccccctgg ctgtgccagg tacggacgcc ctggaccctg
6780
cgaacaggtg gggcgggcga ggggcccagaag ggacgggctc cagagacacg cgccaggcag
6840
gaggggtctc acggaggggt ctcgcactga ggcggccaga gctgggtggtc cggctggacag
6900
ccatccctct gcccgggatc cacacggccc acgtgtgccc gccatgcccgg cgccccacgc
6960
cattgcagtc ttccatccctc tggccgtgac ggtggctgca gttccccat ttgcgcggcgtt
7020
gcctctggct gtctgcactt ttgttcatgc tccaaagaac atttcataat gccttcagta

7080

SequencesSSCPRe-file7August03.ST25.txt

ccgacgtaca cttctgacca ttttgtatgt gtccttgc cgtagtgacc aggcctttt
7140

ttggtgatg tgtaaaaaaa cacactcaa tctcaacttt gtgcaccgtc cattttctag
7200

ggatagacgc ccagggaatg aactctagtt ttctaacaaga ttagctgaga tattaactta
7260

ctcacacgga caggttgatg ccagagccgt aagaatgcgc cagtgcgggt ttgcggggga
7320

cttcgggtgt ggggtcctgc ggccgcgt gcccgtggaaag gttctggggta cccctgctgc
7380

cacggggacg agttcggacg ccaggtggac ctgtgcactc agtaaaacgc agtgattc
7438

<210> 32

<211> 7437

<212> DNA

<213> Homo sapiens

<400> 32

gctgaggcctg agcccgaccc ggggcgcctc ccgcaggca ccgtggtgca gaagtcgcgc
60

aacggcggcg tataaaaaaa cccgagcggg gagaagaagc tgaaggtggg cttcgtgggg
120

ctggaccccg gcgccccga ctccacccgg gacggggcgc tgctgatcgc cggctccgag
180

ccccccaagc gcggcagcat cctcagcaaa cctcgccgg gcggcgcgg cgccggaaag
240

ccccccaagc gcaacgcctt ctaccgcaag ctgcagaatt tcctctacaa cgtgctggag
300

cggccgcgcg gctggcggtt catctaccac gcctacgtgt tcctcctgggt tttctcctgc
360

ctcggtctgt ctgtgttttc caccatcaag gagtatgaga agagctcggg gggggccctc
420

tacatcctgg aaatcgac tatcggtggt tttggcgtgg agtacttcgt gcggatctgg
480

gccgcaggct gctgctgcgg gtaccgtggc tggagggggc ggctcaagtt tgcccgaaaa
540

ccgttctgtg tgattgacat catggtgctc atcgccctca ttgcgggtgt ggccgcggc

SequencesSSCPRe-file7August03.ST25.txt

600

tcccaggggca acgtcttgc cacatctgcg ctccggagcc tgcgcttcct gcagattctg
660

cggatgatcc gcatggaccg gcggggaggc accttggaaac tgctgggctc tgtggtctat
720

gcccacagca aggagctggt cactgcctgg tacatcggt tcctttgtct catcctggcc
780

tcgttcctgg tgtacttggc agagaagggg gagaacgacc actttgacac ctacgoggat
840

gcactctggt ggggcctgat cacgctgacc accattggct acggggacaa gtacccccag
900

accttggaaacg gcaggctcct tgccggcaacc ttcaccctca tcggtgtctc cttttcgcg
960

ctgcctgcag gcatcttggg gtctgggttt gccctgaagg ttcaggagca gcacaggcag
1020

aagcacttt aagaagaggcg gaacccggca gcaggcctga tccagtccgc ctggagattc
1080

tacgccacca acctctcgcg cacagacctg cactccacgt ggcagtacta cgagcgaacg
1140

gtcaccgtgc ccatgtacag ttgccaaact caaacctacg gggcctccag acttatcccc
1200

ccgctgaacc agctggagct gctgaggaac ctcaagagta aatctggact cgctttcagg
1260

aaggaccccc cgccggagcc gtctccaagc cagaaggtca gtttcaaaga tcgtgtttc
1320

tccagcccc gaggcgtggc tgccaaagggg aagggtccc cgcaggccca gactgtgagg
1380

cggtcaccca gcgcggacca gagcctcgag gacagccccca gcaaggtgcc caagagctgg
1440

agcttcgggg accgcagccg ggcacgcccag gcttccgca tcaagggtgc cgctcacgg
1500

cagaactcag aagaagcaag cttccccgga gaggacattt tggatgacaa gagctgcccc
1560

tgcgagttt tgaccgagga cctgaccccg ggcctcaaag tcagcatcag agccgtgtgt
1620

gtcatgcgggt tcctgggttc caagcgaaag ttcaaggaga gcctgcggcc ctacgacgtg
1680

SequencesSSCPRe-file7August03.ST25.txt

atggacgtca tcgagcagta ctcagccgc cacctggaca tgctgtccc 1740
aattaagagc
ctgcagtcca gagtgacca gatcggtggg cggggccca cgatcacgga caaggaccgc 1800
accaaggccc cggccgaggc ggagctgcc gaggacccc gcatgatggg acggctcggg 1860
aagggtggaga agcaggctt gtccatggag aagaagctgg acttccttgtt gaatatctac 1920
atgcagcgg 1980
atgcagcgg 1980
tgggcattttccccc cccgacagag accgaggcct actttggggc caaagagccg
gagccggcgc cggcgtacca cagccggaa gacagccggg agcatgtcga caggcacggc 2040
tgcatgtca agatcg 2100
ccgcgcgcgc cccctgtcca gtgtccgc tccaccttctt ggcagccaca gagccaccc 2160
cgcacggc 2220
ccgcctgc 2280
ttcctgcggc 2340
gacacgtcca tctccatccc gtccgtggac cacgaggagc tggagcgttc cttagcggc 2400
ttcagcatct cccagtc 2460
gcgccttgc 2520
ctctgtaccc cgtgcggc 2580
gtggctggg 2640
ctcctcagca cggcgtcc 2700
agtaactgag tggcggg 2760
agggtggcc ctggaggggc ccatgtggc tgaaggatgg

SequencesSSCPRe-file7August03.ST25.txt
gggctcctgg cagtgaccc ttacaaaagt tattttccaa cagggcaactc ccaggcccctg
2820
tcgccattga ggtgcctccg ctgggctgtc tcctcaccctt tccctgtgt ggagcctgtc
2880
ccaaaaaggt gccaactggg aggccctcgga agccactgtc caggctccca ctgcctgtct
2940
gctctgttcc caaaggcagc gtgtgtggcc tcggggccctg cggtgtggcatg aagcateccct
3000
tctggtgtgg gcatcgctac gtgttttggg ggcagcgttt cacggcggtg cccttgctgt
3060
ctcccttggg ctggctcgag cctgggggtcc atgtcccttt gccgtcccgt catggggcag
3120
ggaatccata gccccggccca caggcagggg tatgagtgcg tcccacccaa cgcagcacca
3180
gccccggccca ccgcgtcccccgt tgcccccaagt tccgtctcag ctacctggac tccaggaccc
3240
tggagaaggg agacctggca gtggagggag gctgtgtgt gtgtccccct gcaggtgtga
3300
ccccgcctgc tctttctc cccgcagggt gtggcccccgc ctgctcttc ctccccccacc
3360
agtatggccc cacctgctct ttccctcccccc cccaaagggt gtggcccccacct gtttttct
3420
ccccctgccga ggtgtgaccc cacctgctct ttccctccctc ccagtatggc cccacctgt
3480
ctttcctccc ccgaggtgag gccccgcctg ctcttctc ccatgggagc cgctgaggcg
3540
tgccgacactg ggcacaggtt ggggctctgc aggatgagga agacaggcca atcccttccc
3600
tcccagaagc tggccggccca gcaggaggga ctgaggccag actcatgtcc agcaaggaac
3660
gtgtgggtgtg tccctggga agtctctggg ccctgggaag agggaaagggtg cactgttgg
3720
gatgggttgcg gggccctgtt ttgggagaca aagggtttaga gggtctgtct tggggccccc
3780
cagactctag. cccgagcagt gcagccaccc actgccccac ctcagagaag tgcagcggga
3840
aggaggctgg aggtggtgcg ggcgtgcctc ggggtgtctgc gtgaatgagc gtggccaagg

3900

SequencesSSCPRe-file7August03.ST25.txt

accagtgcga cctcatggca aagagctccc gcagtgttg ttagagtgcacatcctacgt
3960
gccccactggc acacacacgt gctcacatac atgtccgcgt acaggcgtac acatgcacgc
4020
ttgcacacat gcacacagac cacatagcac acatgtgcac tgaccacacc tgatagacc
4080
atgcacagta cacatacgta catacacatg cctgcataca ggcatacaca tgcacgctta
4140
catgtacacg tgcacagatc acacacatgc acacacgtgt agtcacacaca cagtatacac
4200
atacacaagt gcacagacca cacacagcac taacacatgc acacacaaag tgcataaggcc
4260
acacagcaca tgcacacagg tgcacagacc acacagcaca cacaagtgcac cagagcacac
4320
tgcacacatg cacacacaca cgctgtcatg cacactcctc gcacttccag cttggagcc
4380
cttctgtctc tggtctttct ctggaccct gctgagtgtt agctgcctgg ggaggggcta
4440
caaggagtaa ttgtggctt aggggtcggt gtgatgctgg aatgtcaagc gccgtcggt
4500
ggtatccgac tgtccggct cctggtccgc agtggcagag cgccaggcag agccaatcag
4560
ggtctcggtc tgccttccc cccccacagcc tggcagccat ccagaggagg ggctctacca
4620
gatgccaagg tgccccggtg tctgtatggg tgtccggttt ggtcctgtgt ttggtctgcc
4680
ctggaggtgg ctggccctc ctggatggg tggctcagcc tcgaatccca ggccccagcc
4740
caggcaggtg ctgctgcctg ttgtggtttct ctggcccgac ttctccttct ccctctgtcat
4800
aaaatcacag tccgtgagtc ttccagctgc caccacggct gggacacgct gggggagggc
4860
tcctccatg ctcctgcac acagccgtct gagcaggca ggtgccaaca ccccccaccc
4920
gagacacgct gccccctcagc gatgcccccta cttttgggg ggcctcgctt caageeeeeee
4980

SequencesSSCPRe-file7August03.ST25.txt

cttggaggct gaaatcaccc cagggactgt gagggcttct ccagggggac acccttttag
5040

ctgtgggtct gatcacccca agtcccgcac acggaggaga ggcacagcca gggcgtgtgg
5100

ttaatgttt gcccccttcgg ggctggaggt ctcagtgttt cttagattcca gaccctgctg
5160

ccagagagac ctgctgccgg agagaagggg aggaggactc cagctggct cggtccccca
5220

cagtcaggga cccccataaa ggacacccccc ttctctctag aaagagctgg gctctcagct
5280

atttcttagtt gttcccaaga agccgaggag cagaaggagc tgtgagagct ttgcagaaac
5340

gcccttgcc ccgccttcct gagctatgaa tgccgtacag agcagaggct gggcattgg
5400

caagatcaca ggttgatgct gcacagcccc attgacacaa accctcaaag cagacgtgag
5460

aggacggtt cacaaagctt ggacctgccc tggaggggtgc ccggcagacg tggcgtgaga
5520

gggacggctc acgaggctt gacctgctgt ggaggggtgcc cagcagacgt ggtgtgagag
5580

gaacggctca cgagacttgg acctgggtgga gggtgccca cagacgtggc gtgagaggg
5640

cggctcacag ggcttggacc ggagagagat ggctcatgag acttggacct gccgtggagg
5700

gtgcccagca gacgtggat gagagggatg gtcacgagg cttggacctg gtggaggggtg
5760

ccggcagac gtgtgagagg gacggttcac aaggcttggaa cctgccatgg aggtgccccca
5820

gcagacgtgg tgtgagaggg acagctcacg aggcttggac ctgccgtggaa gggtgccccag
5880

cagggggctg agctctgagg ggtgggtgct cagtgcacgg gtgccccca cttccctctga
5940

tcctgtccgg tgcctccccca aaccccccaca cccatgcaga actcccaggt cacatgcacg
6000

tatgtccagg gcatgggggt ggcgtgaaga ggcctggta gggccttttag gggctgcagg
6060

SequencesSSCPRe-file7August03.ST25.txt
acggaatggc cacctggga gcctgtgtgg ctgtgccggg cagccatctt gcattccccac
6120
ccagcgcgca gtctccacct cggccccagc aaagcgctaa gcagccggag agacagccag
6180
ggcggtttcc tgaaggatgt gggatgggtgg actccgggtt cgagggataa cgcagggttcc
6240
tgtcctccgg gagaccta gaagctgcac acccaggagc ttccatgac ccgggagcat
6300
gagtgaatgg ggggttccag ttgctgaac ttgctgtct tgtaagggtg gggctgacg
6360
gccgaccctg ggaggagggtg acaccgcagg gggagggtgt gggcaacggg ggaggaggag
6420
agacgggagg ggaccatttg ggatggaggg gccttttag agttttaaaa ggcgttttg
6480
gggtggagtt gagtgcttc tggcttggc cacttgcgtt ggtgcccctg gctggccgag
6540
gagactggct ctggccaggg ccccgctctg agaggtcctc agcgtctgac tctggccag
6600
gcgcagcaa ggagggcccg gtccccgggg ctaccaggca ggcacgtgca catcgccatc
6660
gccacacgcc aactccgcct gggtttaca aagtcgttgc cttaatgcat gtggacagga
6720
actccctgag gtcgccccat gccccctggc tgtgccaggt acggacgccc tggaccctgc
6780
gaacaggtgg ggcggcgag gggcccaagg gacgggtcc agagacacgc gcagggcagg
6840
aggggtctca cggaggggtc tcgcactgag ggcggccagag ctgggtggtcc cgctggacgc
6900
catccctctg cccggatcc acacggccca cgtgtgccgg ccatgcccgc gccccacgcc
6960
attgcagtct tccatcctt gcccgtgacg gtggctgcag cttcccatc tgcccggttgc
7020
cctctggctg tctgcacttt tttcatgct ccaaagaaca tttataatg cttcagttac
7080
cgacgtacac ttctgaccat ttgttatgtg tccttgcgc gtagtgcacca ggccttttt
7140
tgggtggatgt gttacccgc acacttcaat ctcaactttg tgcaccgtcc atttcttagg

7200

SequencesSSCPRe-file7August03.ST25.txt

gatagacgcc caggaaatga actctagttt tctaacaagat tagctgagat attaacttac
7260

tcacacggac aggttgatgc cagagccgt aagaatgcgcc agtgcgggtt tgccggggac
7320

ttcgggtgtg gggtcctgcg gccgcgtatgg ccgtggaagg ttctgggat ccctgctgcc
7380

acggggacga gttcgacgc caggtggacc tgtgcactca gtaaaacgca gtgattc
7437

<210> 33

<211> 7437

<212> DNA

<213> Homo sapiens

<400> 33

gctgagcctg agcccgaccc ggggcgcctc ccgcaggca ccacggtgca gaagtcgcgc
60

aacggcggcg tataccccgg cccgagcggg gagaagaagc tgaaggtggg cttcgtgggg
120

ctggaccccg gcgcgcggcga ctccacccgg gacggggcgc tgctgatcgc cggctccgag
180

gcccccaagc gcggcagcat cctcagcaaa cctcgccgg gcggcgcggg cgccgggaag
240

ccccccaagc gcaacgcctt ctaccgcaag ctgcagaatt tcctctacaa cgtgctggag
300

cggccgcgcg gctggcggtt catctaccac gcctacgtgt tcctcctgggt tttctcctgc
360

ctcgtgctgt ctgtgttttc caccatcaag gagtatgaga agagctcggg gggggccctc
420

tacatcctgg aaatcgtgac tatcgtggtg tttggcgtgg agtacttcgt gcggatctgg
480

gcccgcaggct gctgctgccg gtaccgtggc tggagggggc ggctcaagtt tgcccgaaaa
540

ccgttctgtg tgattgacat catggtgctc atcgccctcca ttgcggtgct ggccgcggc
600

tcccaaggca acgtctttgc cacatctgcg ctccggagcc tgcgcttccct gcaagattctg
660

cgatgatcc gcatggaccc gcggggagggc acctggaagc tgctgggctc tgtggtctat

720

SequencesSSCPRe-file7August03.ST25.txt

gcccacagca aggagctggc cactgcctgg tacatcggt tcctttgtct catcctggcc
780

tgcgttcctgg tgtacttggc agagaagggg gagaacgacc actttgacac ctacgcggat
840

gcactctggc ggggcctgat cacgctgacc accattggct acggggacaa gtacccccag
900

accttggAACG gcaggctcct tgcggcaacc ttcaccctca tcggtgtctc cttcttcgat
960

ctgcctgcag gcatcttggg gtctgggttt gccctgaagg ttcaaggagca gcacaggcag
1020

aaggactttg agaagaggcg gaacccggca gcaggcctga tccagtcggc ctggagattc
1080

tacgccacca acctctcgcg cacagacctg cactccacgt ggcagtacta cgagcgaacg
1140

gtcacccgtgc ccatgtacag ttgccaaact caaacctacg gggcctccag acttatcccc
1200

ccgctgaacc agctggagct gctgaggaac ctcaagagta aatctggact cgctttcagg
1260

aaggacccccc cgccggagcc gtctccaagc cagaaggta gtttgaaga tcgtgtctc
1320

tccagccccc gagggcgtggc tgccaaagggg aagggtccc cgccaggccca gactgtgagg
1380

cggtcacccca ggcggcggacc gggcctcgag gacagcccca gcaagggtcc caagagctgg
1440

agcttcgggg accgcagccg ggcacgcccag gctttccgca tcaagggtgc cgcttcacgg
1500

cagaactcag aagaagcaag cctccccggc gaggacattt tggatgacaa gagctgcccc
1560

tgcgagttt tgaccgagga cctgaccccg ggcctcaaaat tcagcatcag agccgtgtgt
1620

gtcatgcggc tcctgggtgc caagcggaag ttcaaggaga gcctgccccttacgacgttg
1680

atggacgtca tcgagcagta ctcagccggc cacctggaca tgctgtcccg aattaagagc
1740

ctgcagtcca gagtgccatca gatcgtgggg cggggcccaag cgatcacggc caaggaccgc
1800

SequencesSSCPRe-file7August03.ST25.txt

accaaggggcc cggccgaggc ggagctgcc gaggaccca gcatgtggg acggctcggg
1860
aagggtggaga agcaggtctt gtccatggag aagaagctgg acttccttgtt gaatatctac
1920
atgcagcggta tggcatccc cccgacagag accgaggcct actttggggc caaagagccg
1980
gagccggcgc cgccgtacca cagccggaa gacagccggg agcatgtcga caggcacggc
2040
tgcatgtca agatcgtcgcttccacgc tccacggcc agaagaactt ctcggcgccc
2100
ccggccgcgc cccctgtcca gtgtccggcc tccacctctt ggcagccaca gagccacccg
2160
cgccaggggcc acggcacctc cccctgtggg gaccacggct ccctgggtcg catccgcgg
2220
ccgcctgccc acgagcggtc gctgtccggcc tacggcgggg gcaaccgcgc cagcatggag
2280
ttcctgcggc aggaggacac cccgggctgc aggccccccg aggggaccct gcgggacagc
2340
gacacgtcca tctccatccc gtccgtggac cacgaggagc tggagcgttc cttagcggc
2400
ttcagcatct cccagtc当地 ggagaacctg gatgtctca acagctgcta cgcggccgtg
2460
gcgccttgc当地 ccaaagtca ggcctacatt gcggagggag agtcagacac cgactccgac
2520
ctctgtaccc cgtgcgggccc cccggccacgc tcggccaccg gcgagggtcc ctgggtgac
2580
gtgggctggg cggggcccaag gaagtggagc ggcgtgggc cagtggaccc gcccgcggcc
2640
ctcctcagca cggtgccctcc gaggtttga ggcgggaacc ctctggggcc ctttcttac
2700
agtaactgag tgtggcgga aggggtggcc ctggaggggc ccatgtggc tgaaggatgg
2760
gggctcctgg cagtgacett ttacaaaagt tattttccaa cagggcactc ccaggccctg
2820
tcggccattga ggtgcctccg ctgggctgtc tcctcacccc tccctgtgct ggagcctgtc
2880

SequencesSSCPRe-file7August03.ST25.txt
ccaaaaagggt gccaactggg aggctcgga agccactgtc caggctccc ctgcctgtct
2940
gctctgttcc caaaggcagc gtgtgtggcc tcgggcccctg cggtggcatg aagcatccct
3000
tctgggtgtgg gcacatcgctac gtgtttgggg ggcagcgttt cacggcggtg cccttgctgt
3060
ctcccccttggg ctggctcgag cctgggggtcc atgtcccttt gccgtcccgt catggggcag
3120
ggaatccata gcggggccca caggcagggg tatgagtgcg tcccacccaa cgcagcacca
3180
gccccggccca ccgctccccg tgtccccagt tccgtctcag ctacctggac tccaggaccc
3240
tggagaaggg agacctggca gtggagggag gctgtgtgt gtgtccccct gcaggtgtga
3300
ccccgcctgc tctttccctcc cccgcccagggt gtggcccccgc ctgctcttc ctccccccacc
3360
agtatggccc cacctgctct ttccctccccc cccaaagggtgt ggccccaccc tttctttccct
3420
cccccgtccga ggtgtgaccc cacctgctct ttccctccctc ccagtatggc cccacctgct
3480
ctttccctccc ccgaggtgag gccccgcctg ctctttccctc ccatgggagc cgctgaggcg
3540
tgcgcacctg ggcacaggtt gggctctgc agatgagga agacaggcca atcccttccc
3600
tcccagaagc tggccggccca gcaggagggc ctgaggccag actcatgtcc agcaaggaac
3660
gtgtgggtgtg tcccctggga agtctctggg ccctgggaag agggaaagggtg cacgtcctgg
3720
gatggttgcg gggccctgtt ttgggagaca aagggtaga gggctgtct tggggccccc
3780
cagactctag cccgagcagt gcagccaccc actgccccac ctcagagaag tgcagcggga
3840
aggaggctgg aggtggtgcg ggcgtgcctc ggggtgtctgc gtgaatgagc gtggccaagg
3900
accagtgccca cctcatggca aagagctccc gcagtgtttgc tttagagtgc aatcctacgt
3960
gcccactggc acacacacgt gtcacatac atgtcccgct acaggcgtac acatgcacgc

4020

SequencesSSCPRe-file7August03.ST25.txt

ttgcacacat gcacacagac cacatagcac acatgtgcac tgaccacacc tgtatagacc
4080

atgcacagta cacatacgtg catabacatg cctgcataca ggcatacaca tgcacgctta
4140

catgtacacg tgcacagatc acacacatgc acacacgtgt agtcacacaca cagtatacac
4200

atacacaagt gcacagacca cacacagcac taacacatgc acacacaaag tgcataggcc
4260

acacagcaca tgcacacagg tgcacagacc acacagcaca cacaagtgc a cagacacac
4320

tgcacacatg cacacacaca cgctgtcatg cacactcctc gcacttccag ccttggagcc
4380

cttctgtctc tggctttct ctggaccct gctgagtgt a gctgcctgg ggaggggcta
4440

caaggagtaa ttgtggctt aggggtcggt gtatgttgg aatgtcaagc gccgtcggt
4500

ggatatccgac tgtccgggct cctggccgc agtggcagag cgccaggcag agccaatcag
4560

ggctcggtgc tgcccttccc cccacagcc tggcagccat ccagaggagg ggctctacca
4620

gatgccaagg tgccccggtg tctgtatggg tgtccgggtt ggtcctgtgt tggctgtcc
4680

ctggaggtgg ctggccctc ctggatggg tggctcagcc tcgaatccca ggccccagcc
4740

cagggcaggc ctgctgcctg ttgtggttc ctggccagc ttctcattct ccctctgcat
4800

aaaatcacag tccgtgagtc ttccagctgc caccacggct gggacacgct gggggagggc
4860

tcctccatg ctcctgcac acagccgtct gagcaggca ggtgccaaca ccccccaccc
4920

gagacacgct gcccctcagc gatgccccta cttttgggg ggcctcgctt caagcccccc
4980

cttggaggct gaaatcaccc caggcactgt gagggcttcc aggggggac accctttgag
5040

ctgtgggtct gatcacccca agtcccgac acggaggaga ggcacagccca gggcgtgtgg
5100

SequencesSSCPRe-file7August03.ST25.txt

ttaatgttt gccccttcgg ggctggaggt ctcagtgtt ctagattcca gaccctgctg
5160

ccagagagac ctgctgccgg agagaagggg aggaggactc cagctggct cggtccccca
5220

cagtcaggga cccccataaa ggacacccccc ttctctctag aaagagctgg gctctcagct
5280

atttctagtt gcttcccaga agccgaggag cagaaggagc tgtgagagct ttgcagaaac
5340

gcccctgtcc ccgcctcct gagctatgaa tgccgtacag agcagaggct ggggcattgg
5400

caagatcaca gtttgatgct gcacagcccc attgacacaa accctcaaaag cagacgtgag
5460

aggacgggtt cacaaagctt ggacctgccg tggaggggtgc cggcagacg tggcgtgaga
5520

gggacggctc acgaggcttg gacctgtgt ggagggtgcc cagcagacgt ggtgtgagag
5580

gaacggctca cgagacttgg acctggtgga gggtgccag cagacgtggt gtgagaggg
5640

cggctcacag ggcttgacc ggagagagat ggctcatgag acttggacct gccgtggagg
5700

gtgcccagca gacgtggat gagagggatg gtcacgagg cttggacctg gtggagggtg
5760

cccgccagac gtgtgagagg gacggttcac aaggcttgga cctgccatgg agggtgccca
5820

gcagacgtgg tgtgagaggg acagctcacg aggcttgac ctgccgtgga gggtgccag
5880

cagggggctg agctctgagg ggtgggtgt cagtgcacgg gtgccccag tgcctctga
5940

tcctgtccgg tgcctccccca aaccccccaca cccatgcaga actcccaggt cacatgcacg
6000

tatgtccagg gcatgggggt ggcgtgaaga ggcctggta gggccttttag gggctgcagg
6060

acggaatggc cacctgggga gcctgtgtgg ctgtgccggg cagccatcct gcattccac
6120

ccagcgcgca gtctccaccc cggcccccagc aaagcgctaa gcagccggag agacagccag
6180

SequencesSSCPRe-file7August03.ST25.txt

ggcggcttcc tgaaggatgt gggatggtgg actccgggtt cgagggaaata cgcaggttcc
6240

tgcctccgg gagacctaga gaagctgcac acccaggagc ttccatgac ccgggagcat
6300

gagtgaatgg ggggttccag ttgctgaac ttgctgtct tgtaagggtg gggctgacg
6360

gccgaccctg ggaggaggtg acaccgcagg gggaggtgt gggcaacggt ggaggaggag
6420

agacgggagg ggaccatttg gatggaggg gcctttcag agtttaaaa ggcgttgc
6480

gggtggagtt gagtgctc tggcttggaa cacttgcgt ggtccccctg gctggccgag
6540

gagactggct ctggccaggg ccccgccctg agaggtcctc agcgtctgac tctcgccag
6600

gcccacgaa ggaggggccc gtcccccggg ctaccaggca ggcacgtgca catcgccatc
6660

gccacacgccc aactccgcct ggttttaca aagtcgttgc cttaatgcat gtggacagga
6720

actccctgag gtcgccccat gccccctggc tgtgccaggt acggacgccc tggaccctgc
6780

gaacaggtgg ggcggcgag gggcccaagg gacgggctcc agagacacgc gcagggcagg
6840

aggggtctca cggaggggtc tcgcactgag ggcggccagag ctgggtgtcc cgctggacgc
6900

catccctctg cccggatcc acacggcca cgttgcccg ccatgcccgc gccccacgccc
6960

attgcagtct tccatccctt ggccgtgacg gtggctgcag cttccatt tggccgttg
7020

cctctggctg tctgcacttt tgccatgct ccaaagaaca tttcataatg cttcagtagc
7080

cgacgtacac ttctgaccat ttgttatgtc tcctgtgcc gtgtgacca ggcctttt
7140

tgggtggatgt gttacccgc acacttaat ctcaactttg tgcaccgtcc atttctagg
7200

gataacgccc cagggaaatga actctagtt tctaacaat tagctgagat attaacttac
7260

tcacacggac aggttgc cagagccgtc agaatgcgc agtgcgggtt tgcggggac

7320

SequencesSSCPRe-file7August03.ST25.txt

ttcgggtgtg gggtcctgcg gcgcgcgtgg ccgtggagg ttctggat ccctgctgcc
7380

acggggacga gtteggacgc caggtggacc tgtgcactca gtaaaacgca gtgattc
7437

<210> 34

<211> 7437

<212> DNA

<213> Homo sapiens

<400> 34

gctgaggctg agcccgaccc ggggcgcctc ccgcaggca ccatggtgca gaagtgcgc
60

aacggggcg tataccccgg cccgagcggg gagaagaagc tgaaggtggg cttcgtggg
120

ctggaccccg ggcgcggcga ctccacccgg gacggggcgc tgctgatgc cgctccgag
180

gcccccaagc gcggcagcat cctcagcaaa cctcgcgcg gcggcgcg ggccggaaag
240

ccccccaagc gcaacgcctt ctaccgcaag ctgcagaatt tcctctacaa cgtgctggag
300

cggccgcgcg gctggcggt catctaccac gcctacgtgt tcctctgggt ttctctgc
360

ctcgtgctgt ctgtgtttc caccatcaag gagtatgaga agagctcgga gggggccctc
420

tacatcctgg aaatcgac tatcggtgg tttggcgtgg agtacttcgt gcggatctgg
480

gcggcaggct gctgctgcgc gtaccgtggc tggagggggc ggctcaagtt tgcccgaaa
540

ccgttctgtg tgattgacat catggtgctc atcgctcca ttgcgggtgc gcccggc
600

tcccaggcga acgtctttgc cacatctgcg ctccggagcc tgcgcttcgt gcagattctg
660

cggatgatcc gcatggaccc gccccggaggc acctggaaagc tgctggctc tgggtctat
720

gccccacagca aggagctggc cactgcctgg tacatcggtc tcctttgtct catcctggcc
780

tcgttcctgg tgtacttggc agagaagggg gagaacgacc actttgacac ctacgcggat

840

SequencesSSCPRe-file7August03.ST25.txt

gcactctgggt ggggcctgat cacgctgacc accattggct acggggacaa gtaccccccag
900
acctggAACG gcagggcct tgcggcaacc ttcaccctca tcggtgtctc cttcttcgCG
960
ctgcctgcAG gcacTttggg gtctgggttt gccctgaagg ttcaGGAGCA gcacaggcAG
1020
aagcacTTG agaAGAGGCG gaACCCGGCA gcaggcCTGA tccAGTCGGC ctggAGATTc
1080
tacGCCacCA acCTCTCGGG cacAGACCTG cACTCCACGT ggcAGTACTA cgAGCgAACG
1140
gtcaccGTGC ccatgtacAG ttCGCAAAct caAAACCTACG gggcCTCCAG acttatcccc
1200
ccgCTGAACC agCTGGAGCT gCTGAGGAAC ctcaAGAGTA aATCTGGACT cgCTTcAGG
1260
aaggACCCCC CGCCGGAGCC gtctccaAGC cagaAGGTCA gtttGAAAGA tcgtgtcttc
1320
tccAGCCCCC gagGCgtggc tgCCAAGGGG aaggGGtccc cgcaggCCCA gactgtgagg
1380
cggtcacCCA gCGCCGACCA gagCCTCGAG gacAGCCCCA gcaAGGTGCC caAGAGCTGG
1440
agCTTCGGGG accGcAGCCG ggcACGCCAG gcttCCGCA tcaAGGGTGC cgCGTCACGG
1500
cagaACTCAG aagaAGCAAG CCTCCCCGGA gaggACATTG tggatGACAA gagCTGCC
1560
tgCGAGTTG tgaccGAGGA CCTGACCCCCG ggCCTCAAAG tcAGCATCAG agCCGTGTGT
1620
gtcAtGCGGT tcctGGTGTc caAGCGGAAG ttcaAGGAGA gcctGCGGCC ctacGACGTG
1680
atggacGTCA tcgAGCAGTA CTCAGCCGGC cacCTGGACA tgCTGTCCC aAttaAGAGC
1740
ctgcAGTCCA gagTGGACCA gatCGTGGGG cggggCCAG cgatCACGGA caaggACCgC
1800
accaAGGGCC CGGCCGAGGC ggAGCTGCC GAGGACCCCCA gcatGATGGG acggCTCGGG
1860
aaggTGGAGA agcAGGTCTT gtccATGGAG aagaAGCTGG actTCCTGGT gaAtATCTAC
1920

SequencesSSCPRe-file7August03.ST25.txt

atgcagcgga tggcatccc cccgacagag accgaggcct actttgggc caaagagccg
1980

gagccggcgc cgccgtacca cagcccgaa gacagccggg agcatgtcga caggcacggc
2040

tgcattgtca agatcgtgcg ctccagcagc tccacggcc agaagaactt ctggcgccc
2100

ccggccgcgc cccctgtcca gtgtccgccc tccacctctt ggcagccaca gagccacccg
2160

cgccagggcc acggcacctc ccccggtggg gaccacggct ccctggtgcg catccgcgg
2220

ccgcctgccc acgagcggtc gctgtccgcc tacggcgggg gcaaccgcgc cagcatggag
2280

ttcctgcggc aggaggacac cccggctgc agggccccc aggggaccct gcgggacagc
2340

gacacgtcca tctccatccc gtccgtggac cacgaggagc tggagcgttc ttccagcggc
2400

ttcagcatct cccagtccaa ggagaacctg gatgtctca acagctgcta cgccggcgtg
2460

gcgccttgtg ccaaagttag gcctacatt gcggagggag agtcagacac cgactccgac
2520

ctctgtaccc cgtgcgggccc cccgccacgc tggccaccc gcgagggtcc ctttggtgac
2580

gtgggctggg ccggggccag gaagttagggc ggctgggc cagtggaccc gcccggcc
2640

ctcctcagca cggcgtcc gaggtttta ggcgggaaacc ctctggggcc ctttcttac
2700

agtaacttag tggcggga aggggtggcc ctggagggc ccatgtggc tgaaggatgg
2760

gggctcctgg cagtgacctt ttacaaaagt tattttccaa cagggcactc ccaggccctg
2820

tcgcattga ggtgcctccg ctgggctgtc tcctcaccctt tccctgtgt ggagcctgtc
2880

ccaaaaagggt gccaactggg aggcctcgga agccactgtc caggctccca ctgcctgtct
2940

gctctgttcc caaaggcagc gtgtgtggcc tcggggccctg cggtggcatg aagcatccct
3000

SequencesSSCPRe-file7August03.ST25.txt
tctgggtgtgg gcacgcgtac gtgtttggg ggcagcggtt cacggcggtg cccttgctgt
3060
ctcccttggg ctggctcgag cctggggtcc atgtccctt gccgtcccgt catggggcag
3120
ggaatccata gcggggccca caggcagggg tatgagtgcg tcccacccaa cgacaccca
3180
ccccccggcca ccgcgtccccg tgtccccagt tccgtctcag ctacctggac tccaggaccc
3240
tggagaaggg agacctggca gtggagggag gctgtgctgt gtgtccccct gcaggtgtga
3300
ccccgcctgc tcttcctcc cccgccaggt gtggcccccgc ctgctcttc ctccccccacc
3360
atatatggccc cacctgctct ttccctccccc cccaaagggtgt ggccccaccc tttttttct
3420
ccctgtccga ggtgtgaccc cacctgctct ttccctccctc ccagtatggc cccacctgct
3480
ctttcctccc ccgaggtgag gccccgcctg ctcttcctc ccatgggagc cgctgaggcg
3540
tgccgcacactg ggcacaggtt ggggtctgc aggatgagga agacaggcca atcccttccc
3600
tcccagaagc tggccgcccc gcaggaggga ctgaggccag actcatgtcc agcaaggaac
3660
gtgtgggtgtg tcccctggga agtctctggg ccctggaaag agggaaagggtg cacgtcctgg
3720
gatggttgcg gggccctgtt ttgggagaca aagggtaga gggtctgtct tgggcccccc
3780
cagactcttag cccgagcagt gcagccacct actgccccac ctcagagaag tgcagcggga
3840
aggaggctgg aggtggtgcg ggcgtgcctc ggggtctgc gtgaatgagc gtggccaagg
3900
accagtggca cctcatggca aagagctccc gcagtgtttt ttagagtgcac catcctacgt
3960
gcccactggc acacacacgt gtcacacatac atgtcccggt acaggcgta acatgcacgc
4020
ttgcacacat gcacacagac cacatagcac acatgtgcac tgaccacacc tgtatagacc
4080
atgcacagta cacatacgtg catacacatg cctgcataca ggcatacaca tgcacgctta

4140

SequencesSSCPRe-file7August03.ST25.txt

catgtacacg tgcacagatc acacacatgc acacacgtgt agtcacaca cagtatacac
4200
atacacaagt gcacagacca cacacagcac taacacatgc acacacaaaag tgcataaggcc
4260
acacagcaca tgcacacagg tgcacagacc acacagcaca cacaagtgc a cagagcacac
4320
tgcacacatg cacacacaca cgctgtcatg cacactcctc gcacttccag cttggagcc
4380
cttctgtctc tggctttct ctggaccct gctgagtgt a gctgcctgg ggaggggcta
4440
caaggagtaa ttgtggctt aggggtcg tgatgctgg aatgtcaagc gccgtcgtgg
4500
ggtatccgac tgtccggct cctggccgc agtggcagag cgccaggcag agccaatcag
4560
ggtctcggtc tgccctccc cccacagcc tggcagccat ccagaggagg ggctctacca
4620
gatgccagg tgccccggtg tctgtatggg tgtccggttg gtcctgtgt ttggctgccc
4680
ctggagggtgg ctggccctc ctggatggg tggctcagcc tcgaatccca ggccccagcc
4740
caggcaggtg ctgctgcctg ttgtggttc ctggcccagc ttctccttct ccctctgcat
4800
aaaatcacag tccgtgagtc ttccagctgc caccacggct gggacacgct gggggagggc
4860
tcctccatg ctcctgcac acagccgtct gagcaggca ggtccaaaca ccccccaccc
4920
gagacacgct gcccctcagc gatgccccta cttttgggg ggcctcgctt caagcccccc
4980
cttggaggct gaaatcaccc caggcactgt gagggcttct ccagggggac accctttgag
5040
ctgtgggtct gatcacccca agtcccgac acggaggaga ggcacagccca gggcgtgtgg
5100
tttaatgttt gccccttcgg ggctggaggt ctcagtgttt ctagattccca gaccctgctg
5160
ccagagagac ctgctgccgg agagaagggg aggaggactc cagctggct cggccccca
5220

SequencesSSCPRe-file7August03.ST25.txt

tcgatgtgga tgagaagaac caaatgatga ccaccaacgt ctggctaaaa caggagtgga
900

gcgactacaa actgcgctgg aaccccgctg atttggcaa catcacatct ctcagggtcc
960

cttctgagat gatctggatc cccgacattg ttctctacaa caatgcagat gggagtttg
1020

cagtgaccca catgaccaag gcccacctct tctccacggg cactgtgcac tgggtgcccc
1080

cgcccatcta caagagctcc tgcagcatcg acgtcacctt cttccccttc gaccagcaga
1140

actgcaagat gaagttggc tcctggactt atgacaaggc caagatcgac ctggagcaga
1200

tggagcagac tgtggacctg aaggactact gggagagcgg cgagtgggcc atcgtcaatg
1260

ccacgggcac ctacaacagc aagaagtacg actgctgcgc cgagatctac cccgacgtca
1320

cctatgcctt cgtcatccgg cggctgccgc tcttctacac catcaacctc atcatcccc
1380

gcctgctcat ctccctgcctc actgtgctgg tcttctacct gcctccgac tgcggcgaga
1440

agatcacgct gtgcatttcg gtgctgctgt cactcaccgt ctccctgctg ctcatcactg
1500

agatcatccc gtccacctcg ctggcatcc cgctcatcg cgagtacctg ctgttcacca
1560

tgcatttcgt caccctgtcc atcgtcatca ccgtcttcgt gctcaatgtg caccaccgct
1620

cccccagcac ccacaccatg ccccactggg tgcggggggc cttctgggc tgtgtgcccc
1680

ggtggtttct gatgaaccgg cccccaccac ccgtggagct ctgccacccc ctacgcctga
1740

agctcagccc ctcttatcac tggctggaga gcaacgtgga tgccgaggag agggaggtgg
1800

tggtgagga ggaggacaga tggcatgtg caggtcatgt ggccccctct gtgggcaccc
1860

tctgcagcca cggccacctg cactctgggg ctcaggtcc caaggctgag gctctgctgc
1920

SequencesSSCPRe-file7August03.ST25.txt

aggaggggtga gctgctgcta tcacccaca tgcagaaggc actggaaggt gtgcactaca
1980

ttgcccgacca cctgcggct gaggatgctg actcttcggt gaaggaggac tgaaagtatg
2040

ttgcccattgtt catcgacagg atcttcctct ggctgtttat catcgctctgc ttcttgggg
2100

ccatcgccct ctttctgcct ccgttccttag ctgaaatgat ctgactgcac ctccctcgag
2160

ctggctcccc gggcaaaggg gagggttctt ggatgtggaa gggcttgaa caatgtttag
2220

atttggagat gagccaaag tgccagggag aacagccagg tgaggtggaa gttggagag
2280

ccaggtgagg tctctctaag tcaggctggg gttgaagttt ggagtctgtc cgagtttgc
2340

gggtgctgag ctgtatggc cagcagggga gtaataaggg ctcttccgga aggggagggaa
2400

gcgggaggca ggcctgcacc tgatgtggag gtacaggcag atcttcctta ccggggaggg
2460

atggatggtt ggatacaggt ggctgggcta ttccatccat ctggaagcac atttggcct
2520

ccaggcttct cttgacgtc attcctctcc ttcttgctg caaaatggct ctgcaccagc
2580

cggcccccag gaggtctggc agagctgaga gccatggcct gcaggggctc catatgtccc
2640

tacgcgtgca gcaggcaaac aaga
2664

<210> 25

<211> 3020

<212> DNA

<213> Homo sapiens

<400> 25

gtcctccgc gggtccgagg gcgctggaaa cccagcggcg gcgaagcggaa gaggagcccc
60

gccccgtctcc gcccccacgg ctccaggtct ggggtctgcg ctggagccgc gcggggagag
120

gccccgtctcg cgaccgcccgc gccccgtctcc gaccgtccgg gtccgcggcc agccccggcca
180

SequencesSSCPRe-file7August03.ST25.txt

cagtcaggga cccccataaa ggacacccccc ttctctctag aaagagctgg gctctcagct
5280

atttcttagtt gtttcccaga agccgaggag cagaaggagc tgtgagagct ttgcagaaac
5340

gcccttgtcc ccgccttcct gagctatgaa tgccgtacag agcagaggct ggggcattgg
5400

caagatcaca gtttgatgct gcacagcccc attgacacaa accctcaaag cagacgttag
5460

agggacggtt cacaaagctt ggacctgccc tggagggtgc ccggcagacg tggcgtgaga
5520

gggacggctc acgaggcttg gacctgtgt ggagggtgcc cagcagacgt ggtgtgagag
5580

gaacggctca cgagacttgg acctggtgga gggtgcccag cagacgttgt gtgagaggg
5640

cggctcacag ggcttggacc ggagagagat ggctcatgag acttggacct gccgtggagg
5700

gtgcccagca gacgttgtat gagagggatg gtcacgagg ctggacactg gtggagggtg
5760

cccgccagac gtgtgagagg gacggttcac aaggcttggaa cttgcacatgg agggtgccca
5820

cgagacgtgg tgtgagaggg acagctcacg aggcttggac ctggcgttgaa gggtgcccag
5880

cagggggctg agctctgagg ggtgggtgct cagtgcacgg gtgcacccag tgtcctctga
5940

tcctgtccgg tgcctcccc aacccccaca cccatgcaga actcccaggt cacatgcacg
6000

tatgtccagg gcatgggggt ggcgtgaaga ggcctggtca gggcttttag gggctgcagg
6060

acggaatggc cacctgggaa gcctgtgtgg ctgtgcgggg cagccatcct gcattccac
6120

ccagcgcgca gtctccaccc cggccccagc aaagcgctaa gcagccggag agacagccag
6180

ggccggcttcc tgaaggatgt gggatggtgg actccgggt cgagggata cgcaggttcc
6240

tgcctccgg gagacctaga gaagctgcac acccaggagc tttccatgac ccgggagcat
6300

SequencesSSCPRe-file7August03.ST25.txt
gagtgaatgg ggggttccag tttgctgaac tttgctgtct tgtaagggtg ggggctgacg
6360
gccgaccctg ggaggaggtg acaccgcagg gggaggttgt gggcaacggt ggaggaggag
6420
agacgggagg ggaccatttg ggatggaggg gcctttcag agttttaaaa ggcgtttgtg
6480
gggtggagtt gagtgtgctc tgggttttggc cacttgcgt ggtccccctg gctggccgag
6540
gagactggct ctggccaggg ccccgtcctg agaggtcctc agcgtctgac tctcgccag
6600
gcccgcagcaa ggagggggccg gtcccccgggg ctaccaggca ggcacgtgca catcgccatc
6660
gccacacgccc aactccgcct gggttttaca aagtcgttgc cttaatgcat gtggacagga
6720
actccctgag gtcgccccat gccccctggc tgtgccaggt acggacgccc tggaccctgc
6780
gaacaggtgg ggcgggcgag gggcccaagg gacgggctcc agagacacgc gcagggcagg
6840
aggggtctca cggaggggtc tcgcacttag ggcgcggcagag ctgggtggtcc cgctggacgc
6900
catccctctg cccgggatcc acacggccca cgtgtccccg ccatgccccgc gccccacgccc
6960
attgcagtct tccatccctt ggcgtgacg gtggctgcag cttccccatt tgcggccgttgc
7020
cctctggctg tctgcacttt tgttcatgct ccaaagaaca tttcataatg ctttcagttac
7080
cgacgtacac ttctgaccat ttgttatgtg tccttgcgc gtagtgcacca ggccttttt
7140
tggtggatgt gttacccgc acacttaat ctcaacttttgcacccgtcc attttctagg
7200
gatacacgccc cagggaaatga actctatgtt tctaacaatgat tagctgagat attaacttac
7260
tcacacggac aggttgatgc cagagccgtt agaatgcgc agtgcgggtt tgcggggac
7320
ttcgggtgtg gggtcctgcg gcccgcgtt ccgtggaaagg ttctggggat ccctgctgc
7380
acggggacga gttcggacgc caggtggacc tgcactca gtaaaacgca gtgattc

7437

SequencesSSCPRe-file7August03.ST25.txt

<210> 35
<211> 7437
<212> DNA
<213> Homo sapiens

<400> 35
gctgagccctg agccccaccc gggggcgccctc ccgcaggca ccatggtgca gaagtcgcgc
60
aacggcggcg tatacccccgg cccgagcggg gagaagaagc tgaagggtggg cttcgtgggg
120
ctggaccccg gcgcgcggcga ctccacccgg gacggggcgc tgctgatcgc cggctccgag
180
gcggccaaagc gcggcagcat cctcagcaaa cctcgccgg gcggcgcggg cgccggaaag
240
ccccccaagc gcaacgcctt ctaccgcaag ctgcagaatt tcctctacaa cgtgctggag
300
cgcccgccgcg gctggcggtt catctaccac gcctacgtgt tcctcctgggt ttctcctgc
360
ctcggtctgt ctgtgttttc caccatcaag gagtatgaga agagctcgg aaaaaaaaaaaaaaaa
420
tacatcctgg aaatcgtgac tatcgtggtg tttggcggtt agtacttcgtt gggatctgg
480
gcggcaggct gctgctgccg gtaccgtggc tggagggggc ggctcaagtt tgcccgaa
540
ccgttctgtg tgattgacat catggtgctc atcgccctcca ttgcgggtgtt gggccggc
600
tcccaggca acgtcttgc cacatctgcg ctccggagcc tgcgtttctt gcagattctg
660
cgatgatcc gcatggaccg gcggggaggc acctggaagc tgctggctc tgggtctat
720
gcggccacagca aggagctggt cactgcctgg tacatggct tcctttgtctt catcctggcc
780
tcgttctgtg tgtacttggc agagaagggg gagaacgacc actttgacac ctacgcccggat
840
gcactctggt gggccctgat cacgctgacc accattggct acggggacaa gtaccccccag
900
acctggaacg gcaggctcct tgcggcaacc ttcaccctca tcgggtgtctc ttcttcggc

960

SequencesSSCPRe-file7August03.ST25.txt

ctgcctgcag gcatcttggg gtctgggtt gccctgaagg ttcaggagca gcacaggcag
1020
aagcacttt agaagaggcg gaaccggca gcaggcctga tccagtcggc ctggagattc
1080
tacgccacca acctctcgcg cacagacctg cactccacgt ggcagtacta cgagcgaacg
1140
gtcaccgtgc ccatgtáacag ttgccaaact caaacctacg gggcctccag acttatcccc
1200
ccgctgaacc agctggagct gctgaggaac ctcaagagta aatctggact cgctttcagg
1260
aaggacccccc cgccggagcc gtctccaagc cagaaggta gtttgaaga tcgtgtcttc
1320
tccagccccct gaggcgtggc tgccaagggg aagggtccc cgcaaggccca gactgtgagg
1380
cggtcacccca ggcggcggcc gagcctcgag gacagccca gcaagggtgcc caagagctgg
1440
agtttcgggg accgcagccg ggcacgcccag gctttccgca tcaagggtgc cgctcacgg
1500
cagaacttag aagaagcaag cctccccgga gaggacattt tggatgacaa gagctgcccc
1560
tgcgagttt tgaccgagga cctgaccccg ggcctcaaag tcagcatcag agccgtgtgt
1620
gtcatgcggt tcctgggtgc caagcggaag ttcaaggaga gcctgcccctacgacgtg
1680
atggacgtca tcgagcagta ctcagccggc cacctggaca tgctgtcccg aattaagagc
1740
ctgcagtcca gagtggacca gatcgtgggg cggggcccg cgatcacgga caaggaccgc
1800
accaaggggcc cggccggaggc ggagctgccc gaggacccca gcatgatggg acggctcggt
1860
aaggtggaga agcaggtctt gtccatggag aagaagctgg acttcctggtaaatatctac
1920
atgcagcggc tgggcattccc cccgacagag accgaggcct actttggggc caaagagccg
1980
gagccggcgc cgccgtacca cagcccgaa gacagccggg agcatgtcga cagggcacggc
2040

SequencesSSCPRe-file7August03.ST25.txt

tgcattgtca agatcgtgcg ctccagcagc tccacgggcc agaagaactt ctcggcgccc
2100

ccggccgcgc cccctgtcca gtgtccgccc tccacacctt ggcagccaca gagccacccg
2160

ccccagggcc acggcacctc ccccgtgggg gaccacggct ccctggtgcg catcccgccg
2220

ccgcctgccc acgagcggtc gctgtccgcc tacggcgggg gcaaccgcgc cagcatggag
2280

ttcctgcggc aggaggacac cccgggctgc aggccccccg aggggaccct gcgggacagc
2340

gacacgtcca tctccatccc gtccgtggac cacgaggagc tggagcgttc cttagcggc
2400

ttcagcatct cccagtc当地 ggagaacctg gatgtctca acagctgcta cgccggccgtg
2460

gcgccttgtg ccaaagtca ggcctacatt gcggagggag agtcagacac cgactccgac
2520

ctctgtaccc cgtgcgggcc cccgccacgc tcggccaccg gcgagggtcc ctttgtgac
2580

gtgggctggg cggggccag gaagtgaggc ggcgctggc cagtggaccc gcccgcggcc
2640

ctcctcagca cggtcctcc gaggtttga ggcgggaacc ctctgggcc ctttcttac
2700

agtaactgag tgtggcgga agggtggcc ctggagggc ccatgtggc tgaaggatgg
2760

gggctcctgg cagtgacatt ttacaaaagt tattttccaa cagggcactc ccaggccctg
2820

tcgccattga ggtgcctccg ctgggctgtc tcctcaccctt tccctgtgct ggagcctgtc
2880

ccaaaaaggt gccaactggg aggccctcgga agccactgtc caggctccca ctgcctgtct
2940

gctctgttcc caaaggcagc gtgtgtggcc tcggggccctg cggtggcatg aagcatccct
3000

tctggtgtgg gcatcgctac gtgtttggg ggcagcgttt cacggcggtg cccttgctgt
3060

ctcccttggg ctggctcgag cctgggggtcc atgtccctt gccgtccctgt catggggcag
3120

SequencesSSCPRe-file7August03.ST25.txt
ggaatccata gcggggccca caggcagggg tatgagtgcg tcccacccaa cgccacca
3180
gccccggcca ccgctcccccgtgtccccactccgtctcag ctacctggac tccaggaccc
3240
tgagaaggaggg agacctggca gtggagggag gctgtgctgt gtgtccccct gcaggtgtga
3300
ccccgcctgc tctttccctcc cccgcacagt gtggcccccgc ctgccttttc ctccccccacc
3360
agatatggccc cacctgctct ttccctccccc cccaaagggtgt ggcccccaccc gttctttccct
3420
ccctgccga ggtgtgaccc cacctgctct ttccctccctc ccagtatggc cccacctgct
3480
cttccctccc ccgaggtgag gccccgcctg ctctttccctc ccatgggagc cgctgaggcg
3540
tgccgcacctg ggcacaggtt ggggtctgc aggatgagga agacaggcca atcccttccc
3600
tcccagaagc tggccgcccgc acaggaggaa ctgaggccag actcatgtcc agcaaggaac
3660
gtgtgggtgtg tccccctggaa agtctctggg ccctggaaag agggaaagggtg cacgtcctgg
3720
gatggttgcg gggccctgtt ttgggagaca aaggggtaga gggctgtct tggccccc
3780
cagactctag cccgagcagt gcagccaccc actgcacccac ctcagagaag tgcagcggga
3840
aggaggctgg aggtgggtgcg ggcgtgcctc ggggtctgc gtgaatgagc gtggccaaagg
3900
accagtgcacccatggca aagagctccc gcagtgttttgc ttagagtgcac catcctacgt
3960
gcccaactggc acacacacgt gtcacacatac atgtccgcgt acaggcgta acatgcacgc
4020
ttgcacacat gcacacagac cacatagcac acatgtgcac tgaccacacc tggatagacc
4080
atgcacagta cacatacgta catabacatg cctgcataca ggcatacaca tgcacgctta
4140
catgtacacg tgcacagatc acacacatgc acacacgtgt agtcacacaca cagtatacac
4200
atacacaagt gcacagacca cacacagcac taacacatgc acacacaaaag tgcataaggcc

4260

SequencesSSCPRe-file7August03.ST25.txt

acacagcaca tgcacacagg tgcacagacc acacagcaca cacaagtgc a cagagcacac
4320

tgcacacatg cacacacaca cgcgtgc atg cacactcctc gcacttccag cttggagcc
4380

cttctgtctc tggtc ttct cttt gaccct gctgagtgt a gctgcctgg ggaggggcta
4440

caaggagtaa ttgtggctt aggggtcg tgatgctgg aatgtcaagc gccgtcg tgg
4500

ggatatccgac tgc cgggct cctggtccgc agtggcagag cgccaggcag agccaatcag
4560

gg tctcg tgc tgc ccccttccc cccacagcc tggcagccat ccagaggagg ggctctacca
4620

gatgccaagg tgccccggtg tctgtatggg tgc cgggtt ggtcctgtgt ttgg tctgcc
4680

ctggagggtgg ctggccctc ctggatggg tggc tca gcc tcgaatccca ggccccagcc
4740

caggcagggtg ctgctgcctg ttgtggttc ctggccagc ttctccctt ccctctgc at
4800

aaaatcacag tccgtgagtc ttccagctgc caccacggct gggacacgct gggggagggc
4860

tccctccatg ctcctgcac acagccgtct gagcaggca ggtgccaaca ccccccaccc
4920

gagaacacgct gcccctc a gatgcccata cttttgggg gcctcg tct caagcccc
4980

cttggaggct gaaatcaccc caggcactgt gagggcttcc tcaggggac accctttgag
5040

ctgtgggtct gatcacccca agtcccgcac acggaggaga ggcacagccca gggcgtgtgg
5100

ttaatgttt gccccttcgg ggctggaggt ctca gtgttt ctagattcca gaccctgctg
5160

ccagagagac ctgctgccgg agagaagggg aggaggactc cagctggct cggccccca
5220

cagtcaggga cccccataaa ggacacccca ttctctctag aaagagctgg gctctcagct
5280

atttcttagtt gcttcccaga agccgaggag cagaaggagc tgtgagagct ttgcagaaac
5340

SequencesSSCPRe-file7August03.ST25.txt

gcccttgc 5400
caagatcaca 5460
aggacgggtt 5520
gggacggctc 5580
gaacggctca 5640
cggtcacac 5700
gtgcccagca 5760
cccgccagac 5820
gcagacgtgg 5880
cagggggctg 5940
tcctgtccgg 6000
tatgtccagg 6060
acggaatggc 6120
ccagcgcgca 6180
ggccggctcc 6240
tgtcctccgg 6300
gagtgaatgg 6360
ggccgaccctg 6420
cogccctcct gagctatgaa tgccgtacag agcagaggct gggcattgg
gcacagecccc attgacacaa accctcaaag cagacgttag
ggacactgccc tggagggtgc ccggcagacg tggcgtgaga
gacctgctgt ggagggtgcc cagcagacgt ggtgtgagag
acctggtgga gggtgcacag cagacgtggt gtgagaggg
ggctcatgag acttggaccc gccgtggagg
gacgtggat gagagggatg gtcacgagg ctggacactg gtggagggtg
aaggcttggaa cctgccatgg agggtgcac
ggctggac 5940
gtgcccagca 5940
actcccac 6000
actcccac 6060
ggcccttttag gggctgcagg
ggccatcct gcattccac
cgagccggag agacagccag
gggcctttag gggctgcagg
cagccatgac ccgggagcat
tttccatgac ccgggagcat
tttgctgaac ttgtgtct tgtaagggtg gggctgacg
gggaggtgt gggcaacgggt ggaggaggag

SequencesSSCPRe-file7August03.ST25.txt

agacgggagg ggaccatttg ggatggaggg gcctttcag agtttaaaa ggcgttgtg
6480

ggtggagtt gagtggtctc tgggcttgg aacttgcgt ggtgccctg gctggccag
6540

gagactggct ctggccaggg ccccgtcctg agaggtcctc agcgtctgac tctcgccag
6600

gccccagcaa ggagggggcg gtccccgggg ctaccaggca ggcacgtgca catcgccatc
6660

gccacacgccc aactccgcct ggttttaca aagtgcgtgc cttaatgcgt gtggacagga
6720

actccctgag gtcgccccat gccccctggc tgtgccaggt acggacgccc tggaccctgc
6780

gaacaggtgg ggcgggcccag gggcccaagg gacgggctcc agagacacgc gcagggcagg
6840

agggtctca cggaggggtc tcgcactgag ggcggccagag ctgggtggcc cgctggacgc
6900

catecctctg cccgggatcc acacggccca cgtgtgcccc ccatgcccgc gccccacgccc
6960

attgcagtct tccatcctct ggccgtgacg gtggctgcag cttcccccatt tgccgcgttg
7020

cctctggctg tctgcacttt tgttcatgct ccaaagaaca tttcataatg cttcagttac
7080

cgacgtacac ttctgaccat tttgtatgtc tccttgcc gtagtgcacca ggccttttt
7140

tggggatgt gttacccgc acacttcaat ctcaactttt tgccacgtcc attttctagg
7200

gatagacgcc caggaaatga actctagtt tctaacaat tagctgagat attaacttac
7260

tcacacggac aggttgatgc cagagccgt aagatgcgcc agtgcgggtt tgccggggac
7320

ttcggtgtg gggcctgctg cccgcgtatgg ccgtggagg ttctggggat ccctgctgcc
7380

acggggacga gttcgacgc caggtggacc tgcactca gtaaaacgcgtt gtttttttt
7437

<210> 36
<211> 7437
<212> DNA

SequencesSSCPRe-file7August03.ST25.txt
<213> Homo sapiens

<400> 36
gctgagcctg agcccgaccc ggggcgcctc ccgccaggca ccatggtgca gaagtgcgc
60

aacggcggcg tataccccgg cccgagcggg gagaagaagc tgaagggtggg cttcgtgggg
120

ctggacccccgg gcgccccga ctccaccggg gacggggcgc tgctgatcgc cggctccgag
180

gcccccaagc gcggcagcat cctcagcaaa cctcgcgcgg gcggcgcggg cgccggaaag
240

ccccccaagc gcaacgcctt ctaccgcaag ctgcagaatt tcctctacaa cgtgctggag
300

cgccgcgcgc gctggcgtt catctaccac gcctacgtgt tcctcctggc tttctcctgc
360

ctcgtgctgt ctgtgttttc caccatcaag gagtatgaga agagctcggg gggggccctc
420

tacatcctgg aaatcgtgac tatcgtggtg tttggcgtgg agtacttcgt gcggatctgg
480

gccgcaggct gctgctgcgg gtaccgtggc tggagggggc ggctcaagtt tgcccgaaa
540

ccgttctgtg tgattgacat catggtgctc atgcctcca ttgcgggtct ggccgcggc
600

tcccaggcga acgtcttgc cacatctgcg ctccggagcc tgcgcttcct gcagattctg
660

cgatgatcc gcatggaccg gcggggagggc acctggaagc tgctggctc tgtggctat
720

gcccacagca aggagctggt cactgcctgg tacatcggt tcctttgtct catcctggcc
780

tcgttctgg tgtacttggc agagaagggg gagaacgacc actttgacac ctacgcggat
840

gcactctggt gggcctgat cacgctgacc accattggct acggggacaa gtaccccccag
900

acctggaacg gcaggctcct tgcggcaacc ttcaccctca tgggtgtctc cttcttcgcg
960

ctgcctgcag gcatcttggg gtctgggttt gcctgaagg ttcaggagca gcacaggcag
1020

aagcactttt agaagaggcg gaacccggca gcaggcctga tccagtcggc ctggagattc

1080

SequencesSSCPRe-file7August03.ST25.txt

tacgccacca acctctcgcg cacagacctg cactccacgt ggcagtacta cgagcgaacg
1140
gtcacccgtgc ccatgtacag ttcgcaaact caaacctacg gggcctccag acttatcccc
1200
ccgctgaacc agctggagct gctgaggaac ctcaagagta aatctggact cgctttcagg
1260
aaggacccccc cgccggagcc gtctccaagc cagaaggtca gtttgaaga tcgtgtcttc
1320
tccagccccc gaggcgtggc tgccaaagggg aagggtccc cgccaggccca gactgtgagg
1380
cggtcaccca gcgcgcacca gacccctcgag gacagcccca gcaagggtgcc caagagctgg
1440
agtttcgggg accgcagccg ggcacgcccag gctttccgca tcaagggtgc cgctcacgg
1500
cagaactcag aagaagcaag cttcccccgg aggacattt tggatgacaa gagctgcccc
1560
tgcgagtttgc tgaccgagga cctgaccccg ggcctcaaag tcagcatcag agccgtgtgt
1620
gtcatgcgggt tcctgggtgc caagcggaag ttcaaggaga gcctgcggcc ctacgacgtg
1680
atggacgtca tcgagcagta ctcagccggc cacctggaca tgctgtcccg aattaagagc
1740
ctgcagtcca gtgtggacca gatcgtgggg cggggcccaag cgatcacggca caaggaccgc
1800
accaaggggcc cggccgaggc ggagctgccc gaggacccca gcatgatggg acggctcgaaa
1860
aagggtggaga agcagggttt gtccatggag aagaagctgg acttcctggta gaatatctac
1920
atgcagcggca tgggcataccc cccgacagag accgaggcct actttggggc caaagagccg
1980
gagccggcgc cgccgtacca cagcccgaa gacagccggg agcatgtcga cagggcacggc
2040
tgcattgtca agatcgtgcg ctccagcagc tccacggcc agaagaactt ctggcgcccc
2100
ccggccgcgc cccctgtcca gtgtccggccc tccaccttctt ggcagccaca gagccaccccg
2160

SequencesSSCPRe-file7August03.ST25.txt

cgccagggcc acggcacctc ccccgtgggg gaccacggct ccctggtgcg catcccgccg
2220

ccgcctgccc acgagcggtc gctgtccgcc tacggcgggg gcaaccgcgc cagcatggag
2280

tccctgcggc aggaggacac cccgggctgc agggccccc aggggaccct gcgggacagc
2340

gacacgtcca tctccatccc gtccgtggac cacgaggagc tggagcgttc cttagcgcc
2400

ttagcatct cccagtc aa ggagaacctg gatgtctca acagctgcta cgccggcgtg
2460

gcgccttgc ccaaagtca ggcctacatt gcggagggag agtcagacac cgactccgac
2520

ctctgtaccc cgtgcgggcc cccggcacgc tcggccaccc gcgagggtcc ctgggtgac
2580

gtgggctggg cggggccag gaagtggggc ggcgtggc cagttggaccc gcccggcc
2640

ctcctcagca cgggcctcc gaggtttga ggcgggaacc ctctgggccc cttttttac
2700

agtaactgag tgtggcggga aggggtggcc ctggagggc ccatgtggc tgaaggatgg
2760

gggctctgg cagtgcaccc ttacaaaat tatttccaa cagggcaccc ccaggccctg
2820

tccgcattga ggtgcctccg ctgggtgtc tccctacccc tccctgtgt ggagcgtgc
2880

ccaaaaaggt gccaactggg aggcctcgga agccactgtc caggctccca ctgcctgtct
2940

gctctgttcc caaaggcagc gtgtgtggcc tcggccctg cggtggcatg aagcatccct
3000

tctgggtgtgg gcatcgctac gtgtttggg ggcagcggtt cacggcggtg cccttgctgt
3060

ctcccttggg ctggctcgag cctgggggtcc atgtccctt ggcgtccctg catggggcag
3120

ggaatccata gcggggccca caggcagggg tatgagtgcg tccccccaa cgcagcacca
3180

gccccggccca cgcgtccctg tgtccccagt tccgtctcag ctacctggac tccaggaccc
3240

SequencesSSCPRe-file7August03.ST25.txt

tggagaaggg agacctggca gtggaggagg gctgtgtgt gtgtccccct gcaggtgtga
3300

ccccgcctgc tctttcctcc cccgccaggt gtggcccccgc ctgctcttc ctccccccacc ..
3360

atatatggccc cacctgctct ttccctcccc cccaagggtgt ggccccaccc gttctttct
3420

ccccctgccga ggtgtgaccgc cacctgctct ttccctccctc ccagtatggc cccacctgct
3480

ctttcctccc ccgaggtgag gccccgcctg ctcttcctc ccatgggagc cgctgaggcg
3540

tgcgcacctg ggcacaggtt ggggctctgc aggatgagga agacaggcca atcccttccc
3600

tcccagaagc tggccgcccc gcaggagggga ctgaggccag actcatgtcc agcaagggaaac
3660

gtgtggtgtg tccccctggga agtctctggg ccctgggaag agggaaagggtg cacgtcctgg
3720

gatggttgcg gggccctgtt ttgggagaca aagggttaga gggtctgtct tggccccc
3780

cagactctag cccgagcagt gcagccaccc actgccccac ctcagagaag tgcagcggga
3840

aggaggctgg aggtggtgcg ggcgtgcctc ggggtgtctgc gtgaatgagc gtggccaagg
3900

accagtgcac aagagctccc gcagtgtttt ttagagtgcac catcctacgt
3960

gcccaactggc acacacacgt gtcacatac atgtccgcgt acaggcgta acatgcacgc
4020

ttgcacacat gcacacagac cacatagcac acatgtgcac tgaccacacc tgtatagacc
4080

atgcacagta cacatacgtg catacacatg cctgcataca ggcatacaca tgcacgctta
4140

catgtacacg tgcacagatc acacacatgc acacacgtgt agtcacacaca cagtatacac
4200

atacacaagt gcacagacca cacacagcac taacacatgc acacacaaaag tgcataaggcc
4260

acacagcaca tgcacacacagg tgcacagacc acacagcaca cacaagtgcac cagagcacac
4320

tgcacacatg cacacacaca cgcgtgcattg cacactcctc gcacttcag ccttggagcc

4380

SequencesSSCPRe-file7August03.ST25.txt

cttctgtctc tggtaaaaaa ctttgacctt gctgagtgtt agctgcctgg ggaggggcta
4440

caaggagtaa ttgtggcttt aggggtcgta gtatgtctgg aatgtcaagc gccgtcgta
4500

ggtatccgac tgtccggct cctggtccgc agtggcagag cgccaggcag agccaatcag
4560

ggtctcgta tgcccttccc cccccacagcc tggcagccat ccagaggagg ggctctacca
4620

gatgccaagg tgccccggta tctgtatggg tgtccggttt ggtccctgtgt ttggctcgcc
4680

ctggaggtgg ctggggccctc ctggggatggg tggctcagcc tcgaatccca ggccccagcc
4740

caggcaggtg ctgctgcctg ttgtggttt ctggcccagc ttctccttct ccctctgcatt
4800

aaaatcacag tccgtgagtc ttccagctgc caccacggct gggacacgct gggggagggc
4860

.tcctcccatg cctcctgcac acagccgtct gagcagggca ggtgccaaca ccccccaccc
4920

gagacacgct gcccctcage gatgcccata cttttgggg gcctcgctt caagcccccc
4980

cttggaggct gaaatcaccc caggcaactgtt gaggcattctt ccagggggac acccttttag
5040

ctgtgggtct gatcacccca agtcccgac acggaggaga ggcacagcca gggcgtgtgg
5100

tttaatgttt gccccttcgg ggctggagggt ctcaatgttt ctatattcca gaccctgctg
5160

ccagagagac ctgctgccgg agagaagggg aggaggactc cagctggct cggcccccc
5220

cagtcaggga cccccataaa ggacacccccc ttctctctag aaagagctgg gctctcagct
5280

atttcttagtt gttcccaaga agccgaggag cagaaggagc tgtgagagct ttgcagaaac
5340

gcccttgccc cggccctcct gagctatgaa tgccgtacag agcagaggct gggcattgg
5400

caagatcaca gtttgatgct gcacagcccc attgacacaa accctcaaag cagacgttag
5460

SequencesSSCPRe-file7August03.ST25.txt

agggacggtt cacaaggctt ggacctgccg tggagggtgc ccggcagacg tggcgtgaga
5520

gggacggctc acgaggcttg gacctgctgt ggagggtgcc cagcagacgt ggtgtgagag
5580

gaacggctca cgagacttgg acctggtgga gggtgcccag cagacgtggt gtgagaggg
5640

cggtcacag ggcttggacc ggagagagat ggctcatgag acttggaccc gccgtggagg
5700

gtgcccagca gacgtggat gagagggatg gtcacgagg cttggaccc gttggagg
5760

ccggcagac gtgtgagagg gacggttcac aaggcttgga cctgccatgg agggtgccca
5820

gcagacgtgg tgtgagaggg acagctcacg aggctggac ctgccgtgg agggtgcccag
5880

cagggggctg agctctgagg ggtgggtgt cagtgcacgg gtgccccag tgtccctctga
5940

tcctgtccgg tgcctccccc aaccccccaca cccatgcaga actcccaggt cacatgcacg
6000

tatgtccagg gcatgggggt ggcgtgaaga ggcctggta gggccttag gggctgcagg
6060

acggaatggc cacctgggaa gcctgtgtgg ctgtgccggg cagccatcct gcattccac
6120

ccagcgcgca gtctccacct cggccccagc aaagcgctaa gcagccggag agacagccag
6180

ggcggcttcc tgaaggatgt gggatgggtgg actccgggggt cgaggaaata cgaggttcc
6240

tgtccctccgg gagacctaga gaagctgcac acccaggagc ttccatgac cccggagcat
6300

gagtgaatgg gggttccag ttgtgtgaac ttgtgtct tgtaagggtg gggctgacg
6360

gccgaccctg ggaggaggtg acaccgcagg gggaggtgt gggcaacggt ggaggaggag
6420

agacgggagg ggaccatgg ggatggaggg gcctttcag agttttaaaa ggcgtttgt
6480

gggtggagtt gagtgtgctc tggcttgga cacttgcgt ggtgcccctg gctggccgag
6540

SequencesSSCPRe-file7August03..ST25.txt

gagactggct ctggccaggc ccccgtcctg agaggtcctc agcgctctgac tctcgccag
6600

gcgccagcaa ggagggggcg gtccccgggg ctaccaggca ggcacgtgca catcgccatc
6660

gccacacgccc aactccgcct gggtttaca aagtgcgtgc cttaatgcatt gtggacagga
6720

actccctgag gtcgccccat gccccctggc tgtgccaggt acggacgccc tggaccctgc
6780

gaacaggtgg ggcgggcgag gggcccaagg gacgggctcc agagacacgc gcagggcagg
6840

aggggtctca cggaggggtc tcgcactgag ggcgcaggag ctggtggtcc cgctggacgc
6900

catccctctg cccgggatcc acacggccca cgtgtgccc ccatgcccgc gccccacgccc
6960

attgcagtct tccatcctct ggccgtgacg gtggctgcag cttccccatt tgccgcgttg
7020

cctctggctg tctgcacttt tgttcatgct ccaaagaaca tttcataatg cttcagtag
7080

cgacgtacac ttctgaccat tttgtatgtg tccttgcc gtagtgacca ggccttttt
7140

tggtggatgt gttacccgc acacttaat ctcaactttg tgcaccgtcc attttctagg
7200

gatagacgcc cagggaaatga actctagttt tctaacaat tagctgagat attaacttac
7260

tcacacggac aggttgatgc cagagccgtc agaatgcgcc agtgcgggtt tgccggggac
7320

ttcgggtgtg gggtcctgcg gccgcgtatgg ccgtggaagg ttctgggat ccctgctgcc
7380

acggggacga gttcggacgc caggtggacc tgcactca gtaaaacgca gtgattc
7437

<210> 37

<211> 7437

<212> DNA

<213> Homo sapiens

<400> 37

gctgagcctg agcccgaccc ggggcgcctc ccgcaggca ccatggtgca gaagtgcgc
60

SequencesSSCPRe-file7August03.ST25.txt

aacggcggcg tataccccgg cccgagcggg gagaagaagc tgaagggtggg cttcgtgggg
120

ctggaccccg ggcgcggcga ctccacccgg gacggggcgc tgctgatcgc cggctccgag
180

gcccccaagc gcggcagcat cctcagcaaa cctcgcgcgg gcggcgcggg cgccggaaag
240

ccccccaagc gcaacgcctt ctaccgcaag ctgcagaatt tcctctacaa cgtgctggag
300

cggccgcgcg gctggcggtt catctaccac gcctacgtgt tcctcctgggt tttctcctgc
360

ctcgtgctgt ctgtgtttc caccatcaag gagtatgaga agagctcggg gggggccctc
420

tacatecctgg aaatcgtgac tatcgtggtg tttggcgtgg agtacttcgt gcggatctgg
480

gccgcaggct gctgctgccc gtaccgtggc tggagggggc ggctcaagtt tgcccgaaa
540

ccgttctgtg tgattgacat catggtgctc atgcctcca ttgcggtgct ggccgcggc
600

tcccaggca acgtcttgc cacatctgcg ctccggagcc tgcgcttcct gcagattctg
660

cggatgatcc gcatggaccg gcggggagggc acctggaagc tgctgggctc tgtggtctat
720

gcccacagca aggagctggt cactgcctgg tacatcggtc tcctttgtct catcctggcc
780

tcgttcctgg tgtacttggc agagaagggg gagaacgacc actttgacac ctacgcggat
840

gcactctggt gggcctgat cacgctgacc accattggct acggggacaa gtaccccaag
900

acctggaacg gcaggctcct tgccggcaacc ttcaccctca tcggtgtctc ctcttcgcg
960

ctgcctgcag gcatcttggg gtctgggttt gccctgaagg ttcaggagca gcacaggcag
1020

aagcactttg agaagaggcg gaacccggca gcaggcctga tccagtcggc ctggagattc
1080

tacgccacca acctctcgcg cacagacctg cactccacgt ggcagtacta cgagcgaacg
1140

gtcaccgtgc ccatgtacag ttgccaaact caaacctacg gggcctccag acttatcccc

SequencesSSCPRe-file7August03.ST25.txt

1200 ccgctgaacc agctggagct gctgaggaac ctcaagagta aatctggact cgctttcagg
1260 aaggacccccc cgccggagcc gtctccaagc cagaaggtaa gtttcaaaga tcgtgtcttc
1320 tccagcccccc gaggcgtggc tgccaaagggg aagggtccc cgccaggccca gactgtgagg
1380 cggtcacccca gcgccgacca gagcctcgag gacagccccca gcaagggtgcc caagagctgg
1440 agcttcgggg accgcagccg ggcacgcccag gctttccgca tcaagggtgc cgctcacgg
1500 cagaactcag aagaagcaag cctccccgga gaggacattt tggatgacaa gagctgcccc
1560 tgcgagttt tgaccgagga cctgaccccg ggccctcaaag tcagcatcag agccgtgtgt
1620 gtcatgcgggt tcctgggttc caagcggaag ttcaaggaga gcctgcccccc ctacgacgtg
1680 atggacgtca tcgagcagta ctcagccggc cacctggaca tgctgtcccg aattaagagc
1740 ctgcagtcca gagtggacca gatcggtggg cggggcccg cgatcacgga caaggaccgc
1800 accaaggggcc cggccgaggc ggagctgccc gaggacccca gcatgatggg acggctcgaaa
1860 aaggtggaga agcagggttt gtccatggag aagaagcgaa acttccgtgtt gaatatctac
1920 atgcagcgga tgggcattccc cccgacagag accgaggcct actttggggc caaagagccg
1980 gagccggcgc cgccgtacca cagcccgaa gacagccggg agcatgtcga caggcacggc
2040 tgcattgtca agatcggtcg ctccagcagc tccacggggcc agaagaactt ctcggcgccc
2100 ccggccgcgc cccctgtcca gtgtccgccc tccacctctt ggcagccaca gagccacccg
2160 cggccaggcc acggcacctc ccccggtggg gaccacggct ccctgggtcg catccgcgc
2220 cccctgtccc acgagcggtc gctgtccggcc tacggcgaaaa gcaaccgcgc cagcatggag
2280

SequencesSSCPRe-file7August03.ST25.txt

ttcctgcggc aggaggacac cccgggctgc aggcggcccg aggggaccct gcgggacagc
2340
gacacgtcca tctccatccc gtccgtggac cacgaggagc tggagcgttc cttcagcggc
2400
ttcagcatct cccagtccaa ggagaacctg gatgctctca acagctgcta cgccggcgtg
2460
gcgccttgc ccaaagtca ggcctacatt gcggagggag agtcagacac cgactccgac
2520
ctctgtaccc cgtgcgggcc cccgccacgc tcggccaccg gcgagggtcc ctttggtjac
2580
gtgggctggg ccggggccag gaagttagggc ggcgcgtggc cagtggaccc gccccggcc
2640
ctcctcagca cggtgccctcc gaggtttga ggcgggaacc ctctggggcc cttttcttac
2700
agtaactgag tgtggcgaaa agggtgggaa ctggaggggc ccatgtgggc tgaaggatgg
2760
gggctcctgg cagtgacatt ttacaaaagt tattttccaa cagggcactc ccaggccctg
2820
tcgcattga ggtgcctccg ctgggctgtc tcctcacccc tccctgtgct ggagcctgtc
2880
ccaaaaaggt gccaactggg aggcctcgaa agccactgtc caggctccca ctgcctgtct
2940
gctctgttcc caaaggcagc gtgtgtggcc tcggccctg cggggcatg aagcatccct
3000
tctggtgtgg gcatcgctac gtgtttggg ggcagcgttt cacggcggtg ccctgtgt
3060
ctcccttggg ctggctcgag cctggggtcc atgtccctt gccgtcccgt catggggcag
3120
ggaatccata gccccggcca caggcagggg tatgagtgcg tcccacccaa cgacgcacca
3180
gccccggcca ccgctcccg tgtccccagt tccgtctcag ctacctggac tccaggaccc
3240
tggagaaggg agacctggca gtggagggag gctgtgtgt gtgtccccct gcaggtgtga
3300
ccccggcctgc tctttcctcc cccggccaggt gtggcccccgc ctgctcttc ctccccacc
3360

SequencesSSCPRe-file7August03.ST25.txt
agtatggccc cacctgctct ttcctccccc cccaagggtgt ggccccacct gttctttcct
3420
cccctgccga ggtgtgaccc cacctgctct ttcctccctc ccagtatggc cccacctgct
3480
cttccctccc ccgaggtgag gccccgcctg ctcttcctc ccatgggagc cgctgaggcg
3540
tgcgcacctg ggcacagggtt ggggctctgc aggatgagga agacaggcca atcccttccc
3600
tcccagaagc tggccgcccc gcaggagggga ctgaggccag actcatgtcc agcaaggaac
3660
gtgtggtgtg tccccctggga agtctctggg ccctggaaag agggaaagggtg cacgtcctgg
3720
gatggttgcg gggccctgtt ttgggagaca aaggggtaga gggctgtct tggggccccc
3780
cagactctag cccgagcagt gcagccacct actgccccac ctcagagaag tgcaagcggga
3840
aggaggctgg aggtggtgcg gcgctgcctc gggtgtctgc gtgaatgagc gtggccaagg
3900
accagtgcac cctcatggca aagagctccc gcagtgtttt ttagagtgc acatcctacgt
3960
gcccaactggc acacacacgt gtcacatac atgtccgcgt acaggcgtac acatgcacgc
4020
ttgcacacat gcacacagac cacatagcac acatgtgcac tgaccacacc tgtatagacc
4080
atgcacagta cacatacgtc catacacatg cctgcataca ggcatacaca tgcacgctta
4140
catgtacacg tgcacagatc acacacatgc acacacgtgt agtcacacaca cagtatacac
4200
atacacaagt gcacagacca cacacagcac taacacatgc acacacaaaag tgcataaggcc
4260
acacagcaca tgcacacagg tgcacagacc acacagcaca cacaagtgcac cagagcacac
4320
tgcacacatg cacacacaca cgcgtgcattg cacactcctc gcacttccag ccttggagcc
4380
cttctgtctc tggtctttct ctttgaccct gctgagtgtt agctgcctgg ggaggggcta
4440
caaggagtaa ttgtggcttt aggggtcggt gtgatgctgg aatgtcaagc gccgtcggtgg

4500

SequencesSSCPRe-file7August03.ST25.txt

ggtatccgac tgtccgggtc cctggtccgc agtggcagag cgccaggcag agccaatcag
4560

ggtctcggtc tgcccttccc cccccacagcc tggcagccat ccagaggagg ggctctacca
4620

gatgccaaagg tgccccggtg tctgtatggg tgtccggttg ggtcctgtgt ttggtctgcc
4680

ctggaggtgg ctggggccctc ctgggatggg tggctcagcc tcgaatccca ggccccagcc
4740

caggcaggtg ctgctgcctg ttgtggtttc ctggcccage ttctccttct ccctctgcat
4800

aaaatcacag tccgtgagtc ttccagctgc caccacggct gggacacgct gggggagggc
4860

tccctccatg ctcctgcac acagccgtct gagcagggca ggtgccaaca ccccccaccc
4920

gagacacgct gccccctcagc gatgccccta ccttttgggg gcctcgctct caagcccccc
4980

cttggaggct gaaatcaccc caggcactgt gagggcttct ccagggggac accctttgag
5040

ctgtgggtct gatcacccca agtccgcac acggaggaga ggcacagcca gggcgtgtgg
5100

tttaatgttt gccccttcgg ggctggaggt ctcagtgttt cttagattcca gaccctgctg
5160

ccagagagac ctgctgccgg agagaagggg aggaggactc cagctggct cggccccca
5220

cagtcaggga cccccataaa ggacacccccc ttctctctag aaagagctgg gctctcagct
5280

atttctagtt gttcccaaga agccgaggag cagaaggagc tgtgagagct ttgcagaaac
5340

gcccttgtcc ccgccttcct gagctatgaa tgccgtacag agcagaggct gggcattgg
5400

caagatcaca ggttcatgtc gcacagccccc attgacacaa accctcaaag cagacgtgag
5460

aggacgggtt cacaaagctt ggacctgccg tggagggtgc ccggcagacg tggcgtgaga
5520

gggacggctc acgaggcttgc acctgtgt ggaggggtgcc cagcagacgt ggtgtgagag
5580

SequencesSSCPRe-file7August03.ST25.txt

gaacggctca cgagacttgg acctggtgga ggggccag cagacgttgt gtgagaggga
5640

cggctcacag ggcttggacc ggagagagat ggctcatgag acttggacct gccgtggagg
5700

gtgcccagca gacgtggtat gagagggatg gtcacgagg cttggacctg gtggagggtg
5760

cccgccagac gtgtgagagg gacggttcac aaggcttggaa cctgccatgg agggtgccca
5820

gcagacgtgg tgtgagaggg acagctcacg aggcttggac ctgcccgttggaa gggtgccag
5880

cagggggctg agctctgagg ggtgggtgct cagtgcacgg gtgccccca gtcctctga
5940

tccctgtccgg tgcctccccc aaccccccaca cccatgcaga actcccaggt cacatgcacg
6000

tatgtccagg gcatgggggt ggcgtgaaga ggcctggtaa gggccttag gggctgcagg
6060

acggaatggc cacctgggaa gcctgtgtgg ctgtgccggg cagccatcct gcattccac
6120

ccagcgcgca gtctccaccc cggcccccagc aaagcgctaa gcagccggag agacagccag
6180

ggcggcttcc tgaaggatgt gggatggtgg actccgggtt cgagggaaata cgaggttcc
6240

tgtcctccgg gagacctaga gaagctgcac acccaggagc ttccatgac ccgggagcat
6300

gagtgaatgg ggggttccag ttgtgtgaac ttgtgtct tgtaagggtg gggctgacg
6360

gccgaccctg ggaggaggtg acaccgcagg gggaggttgt gggcaacgggt ggaggaggag
6420

agacgggagg ggaccatttgg ggtggaggg gcctttcag agttttaaaa ggcgttttgt
6480

gggtggagtt gagtgcttc tggccttggaa cactgtccgt ggtgccccctg gctggccgag
6540

gagactggct ctggccaggg ccccgccctg agaggtcctc agcgtctgac tctcgccag
6600

gcgccagcaa ggaggggcccgtt gtcggggggg ctaccaggca ggcacgtgca catcgccatc
6660

SequencesSSCPRe-file7August03.ST25.txt
gccacacgccc aactccgcct gggttttaca aagtgcgttgc cttaatgcgt gtggacagga
6720

actccctgag gtcgccccat gccccctggc tggccaggt acggacgccc tggaccctgc
6780

gaacagggtgg ggccggcgag gggcccaagg gacgggctcc agagacacgc gcagggcagg
6840

aggggctctca cggaggggtc tcgcactgag gcgcccagag ctggtggtcc cgctggacgc
6900

catccctctg cccgggatcc acacggccca cgtgtgccc ccatgcccgc gccccacgccc
6960

attgcagtct tccatcctct ggccgtgacg gtggctgcag cttccccatt tgccgcgttg
7020

cctctggctg tctgcacttt tttcatgtct ccaaagaaca tttcataatg ctttcagtagc
7080

cgacgtacac ttctgaccat tttgtatgtc tccttgtgcc gtagtgcacca ggccttttt
7140

tggtggatgt gttacccgc acacttcaat ctcaactttt tgccacgtcc attttctagg
7200

gataagacgcc cagggaatga actctagtt tctaacagat tagctgagat attaacttac
7260

tcacacggac aggttgatgc cagagccgt aagatgcgc agtgcgggtt tgccggggac
7320

ttcgggtgtg gggtcctgctg gccgcgtatgg ccgttggagg ttctggggat ccctgctgcc
7380

acggggacga gttcggacgc caggtggacc tgtgcactca gtaaaacgca gtgattc
7437

<210> 38

<211> 169

<212> DNA

<213> Homo sapiens

<400> 38

acttatcccc ccgttgaacc agctggagct gctgaggaac ctcaagagta aatctggact
60

cgctttcagg tcagctgggg agctccaggt gggccgggtg ggcgtctcag tcctggggc
120

cccagctgcc cacagaagac acgccaggac agtgcggccag ggactccag
169

SequencesSSCPRe-file7August03.ST25.txt

<210> 39

<211> 203

<212> DNA

<213> Homo sapiens

<400> 39

atgccggac aggtgacccc atggcggaag acaggggcta tggaatgac ttccccatcg
60

aagacatgtat ccccacccctg aaggccgcca tccgagccgt caggtaatgc ccccacggtc
120

ccacctgtgc ctgtgtgcct cccccactcc agctcaactc ccacaggaag gggcttataaa
180

aattatcttg cactttggga agg
203

<210> 40

<211> 232

<212> DNA

<213> Homo sapiens

<400> 40

aattctacaa ttccgtctct ataaaaaaaa attcaaggag actttgaggc cttacgtatgt
60

gaaggatgtg attgagcagt attctgccgg gcacatcgac atgcttcca ggataaagta
120

ccttcagacg aggtgagaca gtcacatctg gagggactgc actccctca aagccctatg
180

aaccttagag ttttaaggtga gaggtattca gaaataattc aaaatgcagg ga
232

<210> 41

<211> 1925

<212> DNA

<213> Homo sapiens

<400> 41

ggtccattcg ggaattactg cccagcagcc gactaagttt cattcatttga atcttcgcag
60

aaaagacaat tcttttaatc agagtttagta atgtggacag tacaaaatcg agagagtctg
120

gggcttctct ctttccctgt gatgattacc atggctgtt gtgcacacag caccaatgaa
180

cccagcaaca tgccatacgt gaaagagaca gtggacagat tgctcaaagg atatgacatt

cgcttgcggc cggaacttcgg agggcccccc gtcgacgttg ggatgcggat cgatgtcgcc
300
agcatagaca tggtctccga agtgaatatg gattatacac tcaccatgta tttccagcag
360
tcttggaaag acaaaaaggct ttcttattct ggaatcccac tgaacctcac cctagacaat
420
aggtagctg accaactctg ggtaccagac acctacttgc tgaatgacaa gaaatcattt
480
gtgcattgggg tcacagtcaa aaatcgaatg attcgactgc atcctgatgg aacagttctc
540
tatggactcc gaatcacaac cacagctgca tgtatgatgg atcttcgaag atatccattt
600
gatgagcaga actgcaccct ggagatcgaa agttatggct ataccactga tgacattgaa
660
ttttactgga atggaggaga aggggcagtc actgggttta ataaaatcga acttcctcaa
720
tttcaattt ttgactacaa gatgggtct aagaagggtgg agttcacaac aggagcgtat
780
ccacgactgt cactaagttt tcgtctaaag agaaacattt gttacttcat ttgc当地
840
tacatgcctt ctacactgtat tacaattctg tcctgggtgt cttttggat caactatgtat
900
gcatctgcag ccagagtcgc actaggaatc acgacagtgc ttacaatgac aaccatcagc
960
accacacctca gggagaccct gccaaagatc ctttatgtca aagcgattga tatttatctg
1020
atgggttgct ttgtgttgtt gttcctggct ctgctggagt atgcctttgt aaattacatc
1080
ttctttggaa aaggccctca gaaaaaggaa gctagcaaac aagaccagag tgccaatgag
1140
aagaataaac tggagatgaa taaagtccag gtcgacgccc acggtaacat tctcctcagc
1200
accctggaaa tccggaatga gacgagtgcc tcggaagtgc tcacgagcgt gagcgacccc
1260
aaggccacca tgtactccta tgacagcgcc agcatccagt accgcaagcc cctgaggcagc
1320

SequencesSSCPRe-file7August03.ST25.txt

cgcgaggcct acggcgccg cctggaccgg cacgggtac ccagcaaggg gcgcatccgc
1380

aggcgtgcct cccagctcaa agtcaagatc cccgacttga ctgatgtgaa ttccatagac
1440

aagtggtccc gaatgtttt ccccatcacc ttttctttt ttaatgtcg tattggctt
1500

tactatgtac actgaggtct gttctaattgg ttccatattag actactttcc tcttctattg
1560

tttttaacc ttacaggtcc ccaacagcga tactgctgtt tctcgaggtt agagattcag
1620

ccatccaatt ggttttaggt cttgcataatc agtttatta ctgcaccatg tttacttcaa
1680

aaagacaaaa caaaaaaaaaa attattttc cagtcctaccg tggtccaggt tatcagctct
1740

ttaagagctc tattaattgc catgtttaca aacaaacaca aagagagaag ttagacaggt
1800

agatctttag cagtcatttc tagttccct ggatttcact gatttatttt ttagggaaaa
1860

tgaaaagagg accttgctgt ccgcctgcac tgcttcctgg taaactataa, caaacttatg
1920

ctgcc
1925

<210> 42
<211> 1925
<212> DNA
<213> Homo sapiens

<400> 42
ggtccattcg ggaattactg cccagcagcc gactaagttg cattccttga atcttcgcag
60

aaaagacaat tcttttaatc agagtttagta, atgtggacag tacaaaatcg agagagtctg
120

gggcttctct cttccctgt gatgattacc atggctgtt gtgcacacag caccaatgaa
180

cccagcaaca tgccatacgt gaaagagaca gtggacagat tgctcaaagg atatgacatt
240

cgcttgcggc cggacttcgg agggcccccc gtcgacgttg ggatgcggat cgatgtcgcc
300

SequencesSSCPRe-file7August03.ST25.txt

agcatagaca tggctccga agtgaatatg gattatacac tcaccatgt a ttccagcag
360
tcttggaaag acaaaaaggct ttcttattct ggaatcccac tgaacctcac cctagacaat
420
aggtagctg accaactctg ggtaccagac acctacttc tgaatgacaa gaaatcattt
480
gtgcacgggg tcacagtcaa aatcgaatg attcgactgc atcctgatgg aacagttctc
540
tatggactcc gaatcacaac cacagctgca tgtatgatgg atcttcgaag atatccactg
600
gatgagcaga actgcaccct ggagatcgaa agttatggct ataccactga tgacattgaa
660
ttttaactgga atggaggaga aggggcagtc actggtgtt aaaaaatcga acttcctcaa
720
tttcaattt gttactacaa gatggtgtct aagaagggtgg agttcacaac aggagcgtat
780
ccacgactgt cactaagttt tcgtctaaag agaaacattt gttacttcat tttgcaaacc
840
tacatgcctt ctacactgtat tacaattctg tcctgggtgt cttttggat caactatgtat
900
gcacatgcag ccagagtcgc acttaggaatc acgacagtgc ttacaatgac aaccatcagc
960
accacacctca gggagaccct gccaaagatc ctttatgtca aagcgattga tatttatctg
1020
atgggttget ttgtgtttgt gttcctggct ctgctggagt atgcctttgt aaattacatc
1080
ttctttggaa aaggccctca gaaaaaggaa gctagcaaac aagaccagag tgccaatgag
1140
aagaataaac tggagatgaa taaagtccag gtcgacgccc acggtaacat tctcctcagc
1200
accctggaaa tccggaatga gacgagtggc tcggaagtgc tcacgagcgt gagcgacccc
1260
aaggccacca tgtactccta tgacagcgcc agcatccagt accgcaagcc cctgagcagc
1320
cgcgaggcct acgggcgcgc cctggaccgg cacgggtac ccagcaaggg gcgcaccc
1380

SequencesSSCPRe-file7August03.ST25.txt

aggcgtgcct cccagctcaa agtcaagatc cccgacttaa ctgatgtgaa ttccatagac
1440

aagtggtccc gaatgtttt ccccatcacc ttttctctt ttaatgtcgt ctattggcct
1500

tactatgtac actgaggtct gttctaattgg ttccatattag actactttcc tcttctattg
1560

tttttaacc ttacaggtcc ccaacagcga tactgctgtt tctcgaggta agagattcag
1620

ccatccaatt ggttttaggt cttgcataatc agttttatta ctgcaccatg tttacttcaa
1680

aaagacaaaa caaaaaaaaaa attattttc cagtctaccg tggtccaggt tatcagctct
1740

ttaagagctc tattaattgc catgtttaca aacaaacaca aagagagaag ttagacaggt
1800

agatcttttag cagtctttc tagttccct ggatttcact gatttatttt ttagggaaaaa
1860

tgaaaagagg accttgctgt ccgcctgcac tgcttcctgg taaactataa caaacttatg
1920

ctgcc
1925

<210> 43

<211> 1925

<212> DNA

<213> Homo sapiens

<400> 43

ggccatttcg ggaattactg cccagcagcc gactaagttt catttcctga atcttcgcag
60

aaaagacaat tcttttaatc agagttagta atgtggacag tacaaaatcg agagagtctg
120

gggcttcctct ctttccctgt gatgattacc atggctgtt gtgcacacac caccaatgaa
180

cccagcaaca tgccatacgt gaaagagaca gtggacagat tgctcaaagg atatgacatt
240

cgcctgcggc cggacttcgg agggcccccc gtcgacgttg ggatgcggat cgatgtcgcc
300

agcatagaca tggtctccga agtgaatatg gattatacac tcaccatgtt tttccagcag
360

SequencesSSCPRe-file7August03.ST25.txt
tcttggaaag acaaaggct ttcttattct ggaatccac tgaacctcac cctagacaat
420
aggtagctg accaactctg ggtaccagac acctacttc tgaatgacaa gaaatcatt
480
gtgcattttttt tcacagtcaa aaatcgaaatg attcgactgc atcctgatgg aacagttctc
540
tatggactcc gaatcacaac cacagctgca tgtatgatgg atcttcgaag atatccactg
600
gatgacgaga actgcacccct ggagatcgaa agttatggct ataccactga tgacattgaa
660
ttttactgga atggaggaga aggggcagtc actgggttta ataaaatcgaa acttcctcaa
720
tttcaattt ttgactacaa gatgggtct aagaaggtgg agttcacaac aggagcgtat
780
ccacgactgt cactaagttt tcgtctaaag agaaacattt gttacttcat tttgcaaacc
840
tacatgcctt ctacactgat tacaattctg tcctgggtgt ctttttggat caactatgat
900
gcatctgcag ccagagtcgc actaggaatc acgacagtgc ttacaatgac aaccatcagc
960
accCACCTCA gggagacccct gccaaagatc ctttatgtca aagcgattga tatttatctg
1020
atgggttgct ttgtgtttgt gttcctggct ctgctggagt atgctttgt aaattacatc
1080
ttctttggaa aaggccctca gaaaaaggaa gctagcaaac aagaccagag tgccaatgag
1140
aagaataaac tggagatgaa taaagtccag gtcgacgccc acggtaacat tctcctcagc
1200
accctggaaa tccggaatga gacgagtggc tcggaaagtgc tcacgagcgt gagcgacccc
1260
aaggccacca tgtactccta tgacagcgc agcatccagt accgcaagcc cctgagcgc
1320
cgcgaggcct acgggcgcgc cctggaccgg cacgggtac ccagcaaggg ggcgcaccc
1380
aggcgtgcct cccagctcaa agtcaagatc cccgacttga ctgatgtgaa ttccatagac
1440
aagtggtccc gaatgtttt ccccatcacc ttttctcttt ttaatgtcgt ctattggctt

1500

SequencesSSCPRe-file7August03.ST25.txt

tactatgtac actgaggct gttctaattgg ttccattttag actactttcc tcttcttattg
1560

tttttaacc ttacaggtcc ccaacagcga tactgctgtt tctcgaggta agagattcag
1620

ccatccaatt ggttttaggt cttgcatac agtttatta ctgcaccatg tttacttcaa
1680

aaagacaaaa caaaaaaaaaa attattttc cagtctaccg tggtccaggt tatcagctct
1740

ttaagagctc tattaattgc catgtttaca aacaaacaca aagagagaag ttagacaggt
1800

agatctttag cagtctttc tagttccct ggatttcaact gattttttt ttagggaaaa
1860

tggaaaagagg accttgctgt ccgcctgcac tgcttcctgg taaactataa caaacttatg
1920

ctgcc
1925

<210> 44

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 44

tgaattcgtg agatggcgag ctccacggca ccatggcccc gaagctgctg ctccctctct
60

gcctgttctc gggcttgcac gcgcggtcca gaaaggtgga agaggatgaa tatgaagatt
120

catcatcaaa ccaaaagtgg gtcttggctc caaaatccc agacaccgac gtgactctta
180

ttctcaacaa gttgctaaga gagtatgata aaaagctgag gccagatatt ggaataaaac
240

cgaccgtaat tgacgttgac atttatgtta acagcattgg tcctgtgtca tcaataaaca
300

tggaatacca aattgacata tttttgctc agacctggac agatagtcgc ctgcattca
360

acacccatctt ccgcaattctt aaaaccgcag aggctcaactg gatcaccaca cccaatcagc
420

acacccatctt ccgcaattctt aaaaccgcag aggctcaactg gatcaccaca cccaatcagc

480

SequencesSSCPRe-file7August03.ST25.txt

tcctccggat ttggaatgac gggaaaatcc tttacactt gaggctcacc atcaatgctg
540
agtgccagct gcagctgcac aactccccca tggacgaaca ctcctgcccgtcgattttot
600
ccagctatgg ctatccaaa gaagaaatga tttatagatg gagaaaaaat tcagtggagg
660
cagctgacca gaaatcatgg cggctttatc agtttgactt catgggcctc agaaacacca
720
cagaaatcggt gacaacgtct gcaggtgatt atgttgtcat gactataat tttgaattga
780
gtagaagaat gggatacttc accattcaga catacattcc ctgtatactg actgtggttt
840
tatccctgggt gtcattttgg atcaaaaaag atgctacgcc agcaagaaca gcattaggca
900
tcaccacgggt gctgaccatg accaccctga gcaccatcgc caggaagtcc ttgccacgcg
960
tgtcctacgt gaccgccatg gaccttttg tgactgtgtg cttcctgttt gtcttcgcgg
1020
cgctgacgga gtagccacc ctcaactact attccagctg tagaaaacca accaccacga
1080
aaaagacaac atcgttacta catccagatt cctcaagatg gattcctgag cgaataagcc
1140
tacaagcccc ttccaactat tccctcctgg acatgaggcc accaccacct gogatgtca
1200
ctttaaacaat ttccgtttac tggcaggaat ttgaagatac ctgtgtctat gagtgtctgg
1260
atggcaaaga ctgtcagagc ttcttctgtc gctatgaaga atgtaaatca ggatcctgga
1320
ggaaagggcg tattcacata gacatcttgg agctggactc gtactcccggtcgatcc
1380
ccacgtcctt cctgctctt aacctggctc actgggtgg atacctgtat ctctaagtgt
1440
tgctcagagt gaagagtgaa gagcatttgg tacacacttg accttctgtc gtccccagac
1500
cagtagtgac caatcgggag tagcaaggaa ggacac
1536

SequencesSSCPRe-file7August03.ST25.txt

<210> 45
<211> 1843
<212> DNA
<213> Homo sapiens

<400> 45
gcacaattca gaggttaacag cgccctgcgtt ttctccatga taacatagac aaacagttgc
60
ctccaaagct gcagattgga tattgggaag caaatttggg tgtgaaatct tcagcaaagg
120
agcacgcaga gtccatgatg gctcagacca agtgagttag aggcagagcg agggcgcccc
180
tctgctctgg cgcgcggga ctccggactcg cagactcgcg ctggctccag tctctccacg
240
attctctctc ccagactttt ccccggtctt aagagatcct gtgtccagag ggggccttag
300
ctgctccagc ccgcgatgag gaaaagtcca ggtctgtctg actgtcttg ggctggatc
360
ctccttctga gcacactgac tggagaagaac tatggacagc cgtcattaca agatgaactt
420
aaagacaata ccactgtctt caccaggatt ttggacagac tcctagatgg ttatgacaat
480
cgccctgagac caggattggg agagcgtgta accgaagtga agactgatat cttcgtcacc
540
agtttccggac ccgtttcaga ccatgatatg gaatatacaa tagatgtatt ttccgtcaa
600
agcttggagg atgaaaggtt aaaatttaaa ggacctatga cagtcctccg gttaaataac
660
ctaattggcaa gtaaaatccg gactccggac acattttcc acaatggaaa gaagtcagtg
720
gccccacaaca tgaccatgcc caacaaactc ctgcccgtca cagaggatgg caccttgcgt
780
tacaccatga ggctgacagt gagagctgaa tgtccgtgc atttggagga cttccctatg
840
gatccccatg cttgccact aaaatttggaa agttatgctt atacaagagc agaagttgtt
900
tatgaatgga ccagagagcc agcacgctca gtgggtgttag cagaagatgg atcacgtcta
960

SequencesSSCPRe-file7August03.ST25.txt

aaccagtatg accttcttgg acaaacagta gactctggaa ttgtccagtc aagtacagga
1020
gaatatgttg ttatgaccac tcatttccac ttgaagagaa agattggcta ctttgttatt
1080
caaacatacc tgccatgcat aatgacagtg attctctcac aagtctcctt ctggctcaac
1140
agagagtctg taccagcaag aactgtctt ggagtaacaa ctgtgctcac catgacaaca
1200
ttgagcatca gtgccagaaa ctccctccct aaggtggctt atgcaacagc tatggattgg
1260
tttattgccg tgtgcataatgc ctttgttgc tcagctctga ttgagttgc cacagtaaac
1320
tatttcacta agagaggta tgcatggat ggcaaaagtg tggttccaga aaagccaaag
1380
aaagttaaagg atcctcttat taagaaaaac aacacttacg ctccaacagc aaccagctac
1440
acccctaatt tggccagggg cgaccgggc ttagccacca ttgctaaaag tgcaaccata
1500
gaacctaaag aggtcaagcc cgaaacaaaa ccaccagaac ccaagaaaac cttaacagt
1560
gtcagcaaaa ttgaccgact gtcaagaata gccttccgc tgctatttgg aatctttaac
1620
ttagtctact gggctacgta tttaaacaga gagcctcagc taaaagcccc cacaccacat
1680
caatagatct ttactcaca ttctgttgc tcaatgttgc ttatgttgc
1740
ttctcaacgc agtaattccc atctgcctt attgcctcg tcttaagaa ttgaaagtt
1800
tccttattt cataattcat ttaagacaag agaccctgt ctg
1843

<210> 46
<211> 1843
<212> DNA
<213> Homo sapiens

<400> 46
gcacaattca gaggttaacag cgcctgcgtt ttctccatga taacatagac aaacagttgc
60

SequencesSSCPRe-file7August03.ST25.txt

ctccaaagct gcagattgga tattggaaag caaatttggg tgtgaaatct tcagcaaagg
120
agcacgcaga gtccatgatg gtcagacca agtgagttag aggcagagcg aggacgcccc
180
tctgctctgg cgcccccggga ctcggactcg cagactcgcg ctggctccag tctctccacg
240
attctctctc ccagactttt ccccggtctt aagagatcct gtgttcagag ggggccttag
300
ctgctccagc ccgcgatgag gaaaagtcca ggtctgtctg actgtctttg ggcctggatc
360
ctccttctga gcacactgac tggagaaggc tatggacagc cgtcattaca agatgaactt
420
aaagacaata ccactgtctt caccaggatt ttggacagac tcctagatgg ttatgacaat
480
cgcctgagac caggattggg agagcgtgta accgaagtga agactgatat cttcgtcacc
540
agtttcggac ccgtttcaga ccatgatatg gaatatacaa tagatgtatt tttccgtcaa
600
agctggagg atgaaaggtt aaaattaaa ggacctatga cagtcctccg gttaaataac
660
ctaattggcaa gtaaaatccg gactccggac acattttcc acaatggaaa gaagtcagt
720
gcccaacaaca tgaccatgcc caacaaactc ctgcggatca cagaggatgg caccttgctg
780
tacaccatga ggctgacagt gagagctgaa tgtccgatgc atttggagga cttccctatg
840
gatgcccactt cttgcccact aaaatttggaa agttatgctt atacaagagc agaagttgtt
900
tatgaatgga ccagagagcc agcacgctca gtgggtgttag cagaagatgg atcacgtcta
960
aaccagtatg accttcttgg acaaacagta gactctggaa ttgtccagtc aagtacagga
1020
gaatatgtt gatgaccac tcatttccac ttgaagagaa agattggcta ctttgttatt
1080
caaacatacc tgccatgcat aatgacagtg attctctcac aagtctcctt ctggctcaac
1140

SequencesSSCPRe-file7August03.ST25.txt

agagagtctg taccagcaag aactgtcttt ggagtaacaa ctgtgctcac catgacaaca
1200

ttgagcatca gtgccagaaa ctcctccct aagtggtt atgcaacagc tatggattgg
1260

tttatgcccg tgtgctatgc ctttgtgttc tcagctctga ttgagttgc cacagtaaac
1320

tatccacta agagaggta tgcatggat ggcaaaagtg tggttccaga aaagccaaag
1380

aaagtaaagg atcctcttat taagaaaaac aacacttacg ctccaacagc aaccagctac
1440

accctaatt tggccagggg cgaccgggc ttagccacca ttgctaaaag tgcaaccata
1500

gaacctaaag aggtcaagcc cgaaacaaaa ccaccagaac ccaagaaaaac cttaacagt
1560

gtcagcaaaa ttgaccgact gtcaagaata gcctcccgc tgctatttg aatcttaac
1620

ttagtctact gggctacgta tttaaacaga gagcctcagc taaaagcccc cacaccat
1680

caatagatct ttactcaca ttctgttgtt cagttctct gcactggaa tttatattatg
1740

ttctcaacgc agtaattccc atctgcctt attgcctctg tcttaagaa tttgaaagt
1800

tccttatttt cataattcat ttaagacaag agaccctgt ctg
1843

<210> 47

<211> 2189

<212> DNA

<213> Homo sapiens

<400> 47

cctagcgctc ctctccggct tccaccagcc catcgctcca cgctctcttg gctgctgcag
60

tctcggtctc tctctctctc tctctctctc tctctctctc tctctctctc tctctctctc
120

tctctctctc tctctcccaa gtttcctatc tcgtcaagat cagggcaaaa gaagaaaaaca
180

ccgaattctg cttgccgttt cagagcggcg gtgatgaaga caaaattgaa catctacaac
240

SequencesSSCPRe-file7August03.ST25.txt
atcgagttcc tgcttttgt tttcttggtg tggaccctg ccaggttgg gctggctaac
300
atccaagaag atgaggctaa aaataaacatt accatctta cgagaattct tgacagactt
360
ctggatggtt acgataatcg gcttagacca ggactgggag acagtattac tgaagtcttc
420
actaacatct acgtgaccag tttggccct gtctcagata cagatatgga atataacaatt
480
gatgtttct ttcgacaaaa atggaaagat gaacgtttaa aatttaaagg tcctatgaat
540
atccttcgac taaacaattt aatggctagc aaaatctgga ctccagatac ctttttcac
600
aatgggaaga aatcagtagc tcataatatg acaatgccaa ataagttgct tgaattcag
660
gatgatggga ctctgctgta taccatgagg cttacagttc aagctgaatg cccaatgcac
720
ttggaggatt tcccaatgga tgctcattca tgtcctctga aatttggcag ctatgcata
780
acaacttcag aggtcactta tatttgact tacaatgcat ctgattcagt acaggttgct
840
cctgatggct ctaggtaaa tcaatatgac ctgctggcc aatcaatcgg aaaggagaca
900
attaaatcca gtacaggtga atatactgta atgacagctc atttccaccc gaaaagaaaa
960
attgggtatt ttgtgattca aacctatctg ctttgcattca tgactgtcat tctctccaa
1020
gtttcattct ggcttaacag agaatctgtg cctgcaagaa ctgtgtttgg agtaacaact
1080
gtcctaacaa tgacaactct aagcatcagt gctcggatt ctctccccaa agtggcttat
1140
gcaactgcca tggactggtt tattgctgtt tgttatgcat ttgtgttctc tgccctaatt
1200
gaatttgcaa ctgttaatta cttcaccaaa agaggatgga cttggatgg gaagagtgta
1260
gtaaaatgaca agaaaaaaga aaaggcttcc gttatgatac agaacaacgc ttatgcagtg
1320
gctgttgcctt attatgccttcc gaatcttca aaagatccag ttctctccac catctccaaag

1380

SequencesSSCPRe-file7August03.ST25.txt

agtgcacca cgccagaacc caacaagaag ccagaaaaca agccagctga agcaaagaaa
1440

actttcaaca gtgttagcaa aattgacaga atgtccagaa tagtttcc agttttgtt
1500

ggtaacctta atttagttt ctgggctaca tatttaaaca gagaacctgt attaggggtc
1560

agtccttcaa ttgagaccca tgttatctt gggatgtata gcaacattaa atttggtttg
1620

ttttgcatac tacagtctga ctaataactg ctaatttgc atccaacatg tacagtatgt
1680

atatagtgac atagcttacc agtagaccc ttatggagac atgcatttgc taactcatgg
1740

aactgcagac agaaagcact ccatgcgaaa acagccattt cctttttaa agatttaccc
1800

taggaccta tttaaagtga atttcaaattt acctgattaa ttccctattt ttccaaatga
1860

gatgaaaatg gggatcctgt acaaccctt gtggaccctt ttggtttagc tttaagttag
1920

gggtatttt tactgttgct taatttatgtt ggaagataac attgtcattt ctagatgaat
1980

ccttgaagt aacaaacatt gtatctgaca tcagctctgt tcatgagtgc tcagagtccc
2040

tgctaattgtt attgaaagct tggcacat aagaaaaact agagatttga aatctagcta
2100

tgaattactc tatatagtat ctatagccat gtacatatta cagcatgaca agctcgaaat
2160

aattatgagt cagcccgaaa gatgttaat
2189

<210> 48

<211> 2352

<212> DNA

<213> Homo sapiens

<400> 48

gaagatgctg ttgagggccc tggagaaact tcagcagaac .agggccttc cccttgagg
60

ccgagccgca gccctgcgcc ctccccctcc gcccagctcg gccaaggcg catttgctga

120

SequencesSSCPRe-file7August03.ST25.txt

gcgtctggcg gcctctaccg gagcacctct gcagagggcc gatcctccag cccagagacg
180
acatgtggcg ctcggcgag tgccttgcag agagaggagt agcttgctgg ctttgaacgc
240
gtggcggtggc agatatttca gaaagcttca agaacaagct ggagaaggaa agagttattc
300
ctccatattc acctgcttca actactattc ttattggaa tggacaatgg aatgttctct
360
ggttttatca tgatcaaaaa cctccttctc ttttgtatccatgaactt atccagtcac
420
tttggctttt cacagatgcc aaccagttca gtgaaagatg agaccaatga caacatcacg
480
atatttacca ggatcttggaa tgggcttgcg gatggctacg acaacagact tcggccccggg
540
ctgggagagc gcatcactca ggtgaggacc gacatctacg tcaccagctt cggcccggtg
600
tccgacacgg aaatggagta caccatagac gtgttttcc gacaaagctg gaaagatgaa
660
aggcttcgggt ttaaggggcc catgcagcgc ctccctctca acaaccttct tgccagcaag
720
atctggaccc cagacacggtt cttccacaac gggaaagaagt ccatacgctca caacatgacc
780
acgccccaaa agctgctgctg gctggaggac gacggcaccc tgctctacac catgcgcttg
840
accatctctg cagagtgcacc catgcagctt gaggacttcc cgatggatgc gcacgcttgc
900
cctctgaaat ttggcagcta tgcgtaccct aattctgaag tcgtttacgt ctggaccaac
960
ggctccacca agtcgggtggt ggtggcgaa gatggctcca gactgaacca gtaccacctg
1020
atggggcaga cggtgcccac tgagaacatc agcaccagca caggcgaata cacaatcatg
1080
acagctcact tccacctgaa aaggaagatt ggctactttg tcatccagac ctaccttccc
1140
tgataatga ccgtgatctt atcacaggtg tcctttggc tgaaccggaa atcagtcaca
1200

SequencesSSCPRe-file7August03.ST25.txt

gccaggacag tttttgggt caccacggg ctgaccatga cgaccctcag catcagcgcc
1260
aggaactctc tgcccaaagt ggcctacgcc accgccatgg actggttcat agctgtgtgc
1320
tatgccttcg tcttctcggc gctgatagag tttgccacgg tcaattactt taccaagaga
1380
ggctgggcct gggatggcaa aaaagccttg gaagcagcca agatcaagaa aaagcgtgaa
1440
gtcataactaa ataagtcaac aaacgcttt acaactgggaa agatgtctca ccccccaaac
1500
attccgaagg aacagacccc agcagggacg tcgaatacaa cctcagtctc agtaaaaaccc
1560
tctgaagaga agacttctga aagcaaaaag acttacaaca gtatcagcaa aattgacaaa
1620
atgtcccgaa tcgtattccc agtcttgttc ggcactttca acttagttt caaaaatgtt
1680
tatttgaata gggagccggt gataaaagga gccgcctctc caaaataacc ggccacactc
1740
ccaaactcca agacagccat acttccagcg aaatggtacc aaggagaggt tttgctcaca
1800
gggactctcc atatgtgagc actatcttc aggaaatttt tgcatgttta ataataatgtt
1860
caaataatat tgccttgatg tttctatatg taacttcaga tgtttccaag atgtcccatt
1920
gataattcga gcaaacaact ttctggaaaa acaggatacg atgactgaca ctcagatgcc
1980
cagtatcata cgttgatagt ttacaaacaa gatacgtata tttttaactg ctcaagtgt
2040
tacctaacaa tgtttttat acttcaaatg tcatttcata caaattttcc cagtgaaataa
2100
atattttagg aaactctcca tgattattag aagaccaact atattgcgag aaacagagat
2160
cataaagagc acgtttcca ttatgaggaa acttggacat ttatgtacaa aatgaattgc
2220
ctttgataat tcttactgtt ctgaaatttag gaaagtactt gcatgatctt acacgaagaa
2280

SequencesSSCPRe-file7August03.ST25.txt

atagaatagg caaacttta tgtaggcaga ttaataacag aaatacatca tatgttagat
2340

acacaaaata tt
2352

<210> 49
<211> 2352
<212> DNA
<213> Homo sapiens

<400> 49
gaagatgctg ttgagggccc tggagaaaact tcagcagaac agggcctctc cccttgagg
60

ccgagccggg gccctgcgcc ctccccctcc gcccagctcg gccaagggcg cgtttgcga
120

gcgtctggcg gcctctaccg gagcacctct gcagagggcc gatcctccag cccagagacg
180

acatgtggcg ctggggcgag tgccttgcag agagaggagt agcttgctgg ctttgaacgc
240

gtggcgtggc agatatttca gaaagcttca agaacaagct ggagaaggaa agagttattc
300

ctccatattc acctgcttca actactattc ttattggaa tggacaatgg aatgttctct
360

ggtttatca tgatcaaaaa cctccttctc ttttgtatccatgaactt atccagtcac
420

tttggcttt cacagatgcc aaccagttca gtgaaagatg agaccaatga caacatcacg
480

atatttacca ggatcttggaa tggcttttgc gatggctacg acaacagact tcggccggg
540

ctggagagc gcatcacca ggtgaggacc gacatctacg tcaccagctt cggcccggt
600

tccgacacgg aaatggagta caccatagac gtgttttcc gacaaagctg gaaagatgaa
660

aggcttcggt ttaaggggcc catgcagcgc ctccctctca acaacctct tgccagcaag
720

atctggaccc cagacacgtt cttccacaac gggagaagt ccatcgctca caacatgacc
780

acgccccaca agctgctgcg gctggaggac gacggcaccc tgctctacac catgcgcttg
840

SequencesSSCPRe-file7August03_ST25.txt

accatctctg cagagtgc ccc catcagactt gaggacttcc cgatggatgc gcacgcttgc
900

cctctgaaat ttggcagcta tgcgtaccct aattctgaag tcgtttacgt ctggaccaac
960

ggctccacca agtcggtggt ggtggcgaa gatggctcca gactgaacca gtaccacctg
1020

atggggcaga cggtggcac tgagaacatc agcaccagca caggcgaata cacaatcatg
1080

acagctcaact tccacacctgaa aaggaagagg ,ggctactttg tcatccagac ctacaccttcccc
1140

tgcataatga ccgtgatctt atcacaggtg tcctttggc tgaaccggga atcagtccca
1200

gccaggacag tttttgggtt caccacggtg ctgaccatga cgaccctcag catcagcgcc
1260

aggaaactctc tgcccaaagt ggcctacgcc accgcccattgg actggttcat agctgtgtgc
1320

tatgccttcg tcttctcgcc gctgatagag tttgccacgg tcaattactt taccaagaga
1380

ggctgggcct gggatggcaa aaaagccttg gaagcagcca agatcaagaa aaagcgtgaa
1440

gtcataactaa ataagtcaac aaacgctttt acaactggga agatgtctca cccccccaaac
1500

atccgaagg aacagacccc agcagggacg tcgaatacaa cctcagtctc agtaaaaaccc
1560

tcgtgaagaga agacttctga aagcaaaaag actttacaaca gtatcagcaa aattgacaaaa
1620

atgtccccaa tcgtattccc agtctgttc ggcactttca acttagtttta ctgggcaacg
1680

tatggata gggagccgg tataaaagg gcccgccttc caaaaataacc ggccacactc
1740

ccaaatccca agacagccat acttccagcg aaatggtaacc aaggagaggt tttgctcaca
1800

gggatcccc atacgtggc accatccccc aggaaaatttt tgcatgttta ataataatgtt
1860

ccataatatac tgcccttgatg ttttcatatcg taaccttcaga tggtttccaag atgtccatt
1920

1980

SequencesSSCPRe-file7August03.ST25.txt

cagttatcata cggtgatagt ttacaaacaa gatacgtata ttttaactg cttcaagtgt
2040
tacctaacaa tgtttttat acttcaaatg tcatttcata caaatttcc cagtgaataa
2100
atattttagg aaactctcca tgattattag aagaccaact atattgcgag aaacagagat
2160
cataaagagc acgtttcca ttatgaggaa acttgacat ttatgtacaa aatgaattgc
2220
cttgataat tcttactgtt ctgaaattag gaaagtactt gcatgatctt acacgaagaa
2280
atagaatagg caaacttta tgtaggcaga ttaataacag aaatacatca tatgttagat
2340
acacaaaata tt
2352

<210> 50
<211> 2373
<212> DNA
<213> Homo sapiens

<400> 50
gcgcgcggcc cggggcgccgg cgccggagcgg agctgcaggg cggcggcggg agcgcggggc
60
gcaagagccg ctccgcggg agtgcgggg aagttcgcc tggcagcatg gggcggtgac
120
gccgcaccgg cttccgcgc ctgccagccg ggcgagagca ggcggaggag aaggaggatg
180
catcctcacc gacggctcgc ctccccgggc ccgcgcgcag gtgccttgc a gagagaggag
240
tagttgctg gcttgaacg cgtggcgtgg cagatattc agaaagctc aagaacaagc
300
tggagaaggg aagagtatt cctccatatt cacctgcttc aactactatt cttattggga
360
atggacaatg gaatgttctc tgttttatc atgatcaaaa acctccttct cttttgtatt
420
tccatgaact tatccagtca cttggcttt tcacagatgc caaccaggatc agtggaaagat
480
gagaccaatg acaacatcac gatatttacc aggatctgg atgggcttctt ggatggctac

540

SequencesSSCPre-file7August03.ST25.txt

gacaacagac ttccggccgg gctgggagag cgcatcaactc aggtgaggac cgacatctac
600
gtcaccagct tcggcccggt gtccgacacg gaaatggagt acaccataga cgtgttttc
660
cgacaaagct ggaaagatga aaggcttcgg tttaaggggc ccatgcagcg cctccctctc
720
aacaacctcc ttgccagcaa gatctggacc ccagacacgt tcttccacaa cgggaagaag
780
tccatcgctc acaacatgac cacgcccAAC aagctgctgc ggctggagga cgacggcacc
840
ctgctctaca ccatgcgctt gaccatctct gcagagtgcc ccatgcagct tgaggacttc
900
ccgatggatg cgcacgcttg ccctctgaaa ttggcagct atgcgtaccc taattctgaa
960
gtcgttacg tctggaccaa cggtccacc aagtcgggtgg tggcggcgg agatggctcc
1020
agactgaacc agtaccacct gatggggcag acgggtggca ctgagaacat cagcaccaggc
1080
acaggcgaat acacaatcat gacagctcac ttccacactga aaaggaagat tggctacttt
1140
gtcatccaga cctaccTTCC ctgcataatg accgtgatct tatcacaggt gtcctttgg
1200
ctgaaccggg aatcagttccc agccaggaca gttttgggg tcaccacgg gctgaccatg
1260
acgaccctca gcatcagcgc caggaactct ctgccccaaag tggcctacgc caccggcatg
1320
gactggttca tagctgtgtc ctatgccttc gtcttctcg gctgtataga gtttgccacg
1380
gtcaattact ttaccaagag aggctggcc tggatggca aaaaagcctt ggaaggcagcc
1440
aagatcaaga aaaagcgtga agtcataacta aataagtcaa caaacgctt tacaactggg
1500
aagatgtctc acccccccAAA cattccgaag gaacagaccc cagcagggac gtcgaataca
1560
acctcagtctc cagtaaaaacc ctctgaagag aagacttctg aaagcaaaaaa gacttacaac
1620

SequencesSSCPRe-file7August03.ST25.txt

agtatcagca aaattgacaa aatgtcccgta atcgtagttcc cagtcggatggtttcc
1680

aacttagttt actggggcaac gtatttgaat agggagccgg tgataaaaagg agccgcctct
1740

ccaaaataac cgccccacact cccaaactcc aagacagcca tacttccagc gaaatggcac
1800

caaggagagg ttttgctcac agggactctc catatgtgag cactatctt cagggaaattt
1860

ttgcatgttt aataatatgt acaaataata ttgccttgat gtttctatat gtaacttcag
1920

atgtttccaa gatgtcccat tgataattcg agcaaacaac tttctggaaa aacaggatac
1980

gatgactgac actcagatgc ccagtatcat acgtttagat tttacaaaca agatacgtat
2040

attttaact gcttcaagtg ttacctaaca atgtttttt tacttcaaataat gtcatttcat
2100

acaaattttc ccagtgaata aatatttttag gaaactctcc atgattatta gaagaccaac
2160

tatattgcga gaaacagaga tcataaagag cacgtttcc attatgagga aacttggaca
2220

tttatgtaca aatgaatttgc cctttgataa ttcttactgt tctgaaatttta ggaaagtact
2280

tgcgtatct tacacgaaga aatagaatag gcaaactttt atgttaggcag attaataaca
2340

gaaatacatac atatgtttaga tacacaaaaat att
2373

<210> 51

<211> 1974

<212> DNA

<213> Homo sapiens

<400> 51

cgcgcggggaa agggagaag aggacgagggt ggcgcagaga cgcggggaga acacagtgt
60

tccggaggaa atctgctcggtcccccggcag ccgcgttcc cctttgatgt tttggtaacgc
120

cgtggccatg cgccctcacat tagaattact gcactggca gactaagggtg gatctcctct
180

SequencesSSCPRe-file7August03.ST25.txt

cttcagtcaa accctaatt ccatcaaaaa ctaaaggat gtggagagtc cgaaaaaggg
240

gctactttgg gatttggtcc ttccccttaa taatcgccgc tgtctgtgcg cagagtgtca
300

atgaccctag taatatgtcg ctggtaaaag agacggtgga tagactcctg aaaggctatg
360

acattcgtct gagaccagat tttggaggtc cccccgtggc tgtggggatg aacattgaca
420

ttgccagcat cgatatggtt tctgaagtca atatggatta taccttgaca atgtacttgc
480

aacaaggctg gagagataag aggctgtcct ataatgtaat acctttaaac ttgactctgg
540

acaacagagt ggcagaccag ctctgggtgc ctgataccta tttcctgaac gataagaagt
600

catttgtca cggagtgact gtttagaacc gcatgattcg cctgcattct gatggcaccc
660

tcctttatgg actcagaatc acaaccacag ctgcctgcat gatggaccta aggaggtacc
720

cactggatga acaaaactgc accttggaaa ttgagagcta tggatacaca actgatgaca
780

tttagttta ctggcgtggc gatgataatg cagtaacagg agtaacgaaa attgaacttc
840

cacagttctc tattgttagat tacaaactta tcaccaagaa gttttttt tccacaggtt
900

cctatcccag gttatccctc agctttaagc ttaagagaaa cattggctac tttatcctgc
960

aaacatacat gcttccatc ctgattacca tccttcctc ggtctccttc tggattaatt
1020

acgtgcttc agctgcaagg gtggcattag gaatcacaac tgtcctcaca atgaccacaa
1080

tcaacaccca cctccggaa actctcccta aaatccccta tgtgaaggcc attgacatgt
1140

acctgatggg gtgctttgtc ttctttca tggcccttct ggaatatgcc ctatgtcaact
1200

acatcttctt tgggaggggg ccccaacgccc aaaagaaaagc agctgagaag gctgccagtg
1260

SequencesSSCPRe-file7August03.ST25.txt

ccaacaatga gaagatgcgc ctggatgtca acaagattt ttataaaagat attaaacaaa
1320

atgggaccga atatcgatcc ttgtgggacc ctactggaaa cctctccca actagacgga
1380

ctaccaatta cgatttctct ctgtatacga tggacccca tgagaacatc ttactgagca
1440

ctctcgagat aaaaaatgaa atggccacat ctgaggctgt gatgggactt ggagacccca
1500

gaagcacaat gctagcctat gatgcctcca gcatccagta tcggaaagct gggttgccc
1560

ggcatagttt tggccgaaat gctctggaac gacatgtggc gcaaaagaaa agtcgcctga
1620

ggagacgcgc ctcccaactg aaaatcacca tccctgactt gactgatgtg aatgccatag
1680

atcggtggtc ccgcataattc ttcccagtgg tttttcctt cttcaacatc gtctattggc
1740

tttactatgt gaactaaaca tggcctccca ctggaagcaa ggactagatt ctcctcaaa
1800

ccagttgtac agcctgatgt aggacttggaa aaacacatca atccaggaca aaagtgacgc
1860

taaaataacct tagttgctgg cctatcctgt ggtccatttc ataccatttg gtttgcttct
1920

gctaagtaat gaatacacta aggtccttgtt ggtttccag taaaacgca agta
1974

<210> 52

<211> 1974

<212> DNA

<213> Homo sapiens

<400> 52

cgcgcgggaa aggaaagaag aggacgaggt ggcgcagaga ccgcgggaga acacagtggc
60

tccggaggaa atctgctcggtccccggcag ccgcgttcc ctttgcattgt tttggtagc
120

cgtggccatg cgcctcacat tagaattact gcactggca gactaaggat gatctcctct
180

cttcagtgaa accctcaatt ccatcaaaaa ctaaaggat gtggagagtc cggaaaagg
240

SequencesSSCPre-file7August03.ST25.txt
gctactttgg gatttggtcc ttcccccttaa taatcgccgc tgtctgtgcg cagagtgtca
300
atgaccctag taatatgtcg ctgggtaaag agacggtgga tagactcctg aaaggctatg
360
acattcgtct gagaccagat tttggaggtc cccccgtggc tgtggggatg aacattgaca
420
ttgccagcat cgatatggtt tctgaagtca atatggatta taccttgaca atgtactttc
480
aacaaggctg gagagataag aggctgtcct ataatgtaat acctttaaac ttgactctgg
540
acaacagagt ggcagaccag ctctgggtgc ctgataccta tttcctgaac gataagaagt
600
catttgtca cggagtgact gtttagaacc gcatgattcg cctgcattct gatggcacccg
660
tcctttatgg actcagaatc acaaccacag ctgcctgcat gatggaccta aggaggtacc
720
cactggatga acaaaaactgc accttggaaa ttgagagcta tggatacaca actgatgaca
780
ttgagttta ctggcgtggc gatgataatg cagtaacagg agtaacgaaa attgaacttc
840
cacagtttctc tattgttagat tacaactta tcaccaagaa gtttggtttt tccacaggtt
900
cctatcccag gttatccctc agcttaagc ttaagagaaa cattggctac tttatcctgc
960
aaacatacat gccttccatc ctgattacca tccttcctg ggtctccttc tggattaatt
1020
acgatgcttc agctgcaagg gtggcattag gaatcacaac tgtcttcaca atgaccacaa
1080
tcaacaccca cctccggaa acttcctca aaatcccata tgtgaaggcc attgacatgt
1140
acctgtatggg gtgtttgtc ttctttca tggcccttc ggaatatgcc ctatgtcaact
1200
acatcttctt tgggagggggg ccccaacgccc aaaagaaaagc agctgagaag gctgccagtg
1260
ccaacaatga gaagatgcgc ctggatgtca acaagattt ttataaagat attaaacaaa
1320
atgggaccca atatcgatcc ttgtgggacc ctactggaaa ccttcacca actagacgga

1380

SequencesSSCPre-file7August03.ST25.txt

ctaccaatta cgatttctct ctgtatacga tggaccccca tgagaacatc ttactgagca
1440

ctctcgagat aaaaaatgaa atggccacat ctgaggctgt gatgggactt ggagacccca
1500

gaagcacaat gctagcctat gatgcctcca gcatccagta tcggaaagct gggttgccca
1560

ggcatagttt tggccgaaaat gctctggaac gacatgtggc gcaaaagaaa agtcgcctga
1620

ggagacgcgc ctcccaactg aaaatcacca tccctgactt gactgatgtg aatgccatag
1680

atcggtggtc ccgcataattc ttcccagtgg tttttcctt cttcaacatc gtctattggc
1740

tttactatgt gaactaaaca tggcctcca ctggaagcaa ggactagatt cctcctcaaa
1800

ccagttgtac agcctgatgt aggacttggaa aaacacatca atccaggaca aaagtgacgc
1860

taaaataacct tagttgctgg cctatcctgt ggtccatttc ataccatttg ggttgcttct
1920

gctaagtaat gaatacacta aggtccttgtt ggtttccag ttaaaatgca agta
1974

<210> 53

<211> 3282

<212> DNA

<213> Homo sapiens

<400> 53

ggcacagggc tgaggatgag gagaaccctg gggacccaga agaccgtgcc ttgcctggaa
60

gtcctgcctg taggcctgaa ggacttgccc taacagagcc tcaacaacta cctggatt
120

cctacttcag ccccttggtg tgagcagctt ctcaacatga actacagcct ccacttggcc
180

ttcgtgtgtc tgagtctctt cactgagagg atgtgcattc aggggagtc gttcaacgtc
240

gaggtcggca gaagtgacaa gctttccctg cctggcttg agaacctcac agcaggat
300

aacaaatttc tcaggccaa ttttggtggaa gaaccgtac agatagcgct gactctggac

SequencesSSCPRe-file7August03.ST25.txt

360

attgcaagta tctctagcat ttcagagagt aacatggact acacagccac catatacctc
420

—

cgacagcgct ggatggacca gcggctggtg tttgaaggca acaaagagctt cactctggat
480

卷之三

ccctc
688

ctgtatcccc tcagaatcac gacaactgtt gcatgtaca tggatctgtc taaatacccc
660

660

atggacacac agacatgcaa gttgcagctg gaaagctggg gctatgatgg aaatgatgtg
720

780

ngtac

tacactagat tggtcttaca gtttgagctt cgaggaaatg ttctgtattt cattttggaa

900

accttacgttc ctccacttt cctgggtggtgg tttcattttg gatctcttc
960

2

gattcagtcc ctgcaagaac ctgcatttgg a gtcacgaccg ttttatcaat gaccacactg
1020

838

1080 tacctgggaa tctgttttag cttttgtttt gggttgttgc tagaatatgc acttgatcag

140

tacagttcct tacagcagat ggcagccaaa gataggggga caacaaagga agtagaagaa
1200

200

gtcagtattt ctaatatcat caacagctcc atctccagct ttaaacggaa gatcagcttt
1260

1320

caac

aaaaacccca gttatgttgc tggatatttcg aaactgtat ttttttttgtt tttttgtata

aaaac
140

SequencesSSCPRe-file7August03.ST25.txt

gccaatgtat tttactggc atactacatg tatttttag tcaatgtaa atttcttgc
1500

tgcctatagg cttaaacagg acaagataat gatgtaaatg gtattttagg ccaagtgtgc
1560

accacatcc aatggtgcta caagtgactg aaataatatt tgagtcttc tgctcaaaga
1620

atgaagctcc aaccatgtt ctaagctgtg tagaagtccct agcattatacgatcttgc
1680

tagaaacatc agtccattcc tctttcatct taatcaagga cattccatg gagcccaaga
1740

ttacaaatgt actcagggct gtttattcgg tggctccctg gtttgcattt acctcatata
1800

aagaatggga aggagaccat tggtaaccc tcaagtgtca gaagttgttt ctaaagtaac
1860

tatacatgtt ttactaaa tcctgcagt gcttataaaa tacattgttgcctatgg
1920

gagtaacatt ttctagttt tggctgggt taaaatgaaa tatggctta tgtcaattca
1980

ttggaaagtca atgcactaac tcaataccaa gatgagttt taaataatga atattatca
2040

ataccacaac agaattatcc ccaatttcca ataagtccta tcattgaaaa ttcaaatata
2100

agtgaagaaa aaatttagtag atcaacaatc taaacaaatc cctcggttct aagataacaat
2160

ggattccccca tactggaagg actctgaggc tttattcccc cactatgcattatcat
2220

tttatttata tacacacatc catcctaaac tatactaaag ccctttccc atgcattggat
2280

ggaaatggaa gatTTTTG taacttgcattt tagaagtctt aatatggct gttgccatga
2340

aggcttgcag aattgagtcc attttcttagc tgcctttatt cacatagtga tgggtacta
2400

aaagtaactgg gttgactcag agagtcgctg tcatttgcattt cacatagtga tgggtacta
2460

gagcaacact ctcccagtgg cagatcccct gtatcattcc aagaggagca ttcatccctt
2520

SequencesSSCPre-file7August03.ST25.txt

tgctctaatt atcaggaatg atgcatttatta gaaaacaaac tgcttgaccc aggaacaagt
2580

ggcttagctt aagtaaactt ggctttgctc agatccctga tccttccagc tggctcgctc
2640

tgagtggctt atccccatg agcaggagcg tgctggccct gagtaactgaa ctttctgagt
2700

aacaatgaga cacgttacag aacctatgtt caggttgcgg gtgagctgcc ctctccaaat
2760

ccagccagag atgcacattc ctcggccagt ctcagccaac agtaccaaaa gtgatttttg
2820

agtgtgccag ggttaaaggct tccagttcag cctcagttat tttagacaat ctgcctatct
2880

ttaatttctt agtttcctgt tctaataaat gcacggctt acctttcctg tcagaaataa
2940

accaaggctc taaaagatga tttcccttct gtaactccct agagccacag gttctcatc
3000

cttttcccat tataacttctc acaattcagt ttctatgagt ttgatcacct gatTTTTTA
3060

acaaaatatt tctaacggga atgggtggga gtgctggta aaagagatga aatgtggttg
3120

tatgagccaa tcataatttgt gatTTTTAA aaaaagTTA aaaggaaata tctgttctga
3180

aaccccactt aagcattgtt tttatataaa aacaatgata aagatgtgaa ctgtgaaata
3240

aatataccat attagctacc caccaaaaaa aaaaaaaaaa aa
3282

<210> 54

<211> 270

<212> DNA

<213> Homo sapiens

<400> 54

ggtccattcg ggaattactg cccagcagcc gactaagttt cattccttga atcttcgcag
60

aaaagacaat tcttttaatc agagtttagta atgtggacag tacaaaatcg agagagtctg
120

gggcttctct cttccctgt gatgattacc atggctgtt gtgcacacag gtgagctgct
180

SequencesSSCPRe-file7August03.ST25.txt

gttgttgaat ctcgctctct ctctctcttt ttttcttggt atgtttcttt ttacgtgtct
240

gctggatcat gtatcttgtt gtttgggggt
270

<210> 55
<211> 238
<212> DNA
<213> *Homo sapiens*

<400> 55
atggctatac cactgatgac attgaatttt actggaatgg aggagaaggg gcagtcactg
60

gtgttaataa aatcgaactt cctcaatttt caattgttga ctacaagatg gtgtctaaga
120

aggtggagtt cacaacaggt gaggttgttt ccccaaaat gtactagggg tgctgtgaaa
180

ggaagaagat gttccaaacc aaataatggg ctgattactt gtctttgtt tctcaact
238

<210> 56
<211> 345
<212> DNA
<213> *Homo sapiens*

<400> 56
gcaccaataa ggaagtggca aatggcatct gtcctctcaa tcttgaaaaaa ggaacttaat
60.

agtggcgccct tcagctaagt gttgttttc tctttcacag gaatcacgac agtgcttaca
120

atgacaacca tcagcaccca cctcaggag accctgc₁₈₀ agatccctta tgtcaaagcg

atttatattt atctgatggg ttgttttgtg tttgtgttcc tggctctgct ggagtatgcc
240

tttgtaaatt acatcttctt tgggaaaaggc cctcagaaaa agggagctag caaacaagac
300

cagagtggcca atgagaagaa taaactggag atgaataaaag tccag
345 .

<210> 57
<211> 190
<212> DNA
<213> *Homo sapiens*

SequencesSSCPRe-file7August03.ST25.txt

<400> 57
gggtggccg gcgggcggcg ggcagggcgc ggggtgcgcg gggcgctggc ggctgagccg
60

ccctgaccc cgctcttgcgtc ctcctccat tgtgaacgat cccggaaaca
120

tgcctttgt gaaggagacg gtggacaagg tggtaaaagg ctacgacatt cgcctaagac
180

ccgacttcgg
190

<210> 58

<211> 253

<212> DNA

<213> Homo sapiens

<400> 58

gtgcctatcc tcgactgtca ctgagcttc gttgaagag gaacatttga tacttcattc
60

ttcagactta tatgccctct atactgataa cgattctgtc gtgggtgtcc ttctggatca
120

attatgatgc atctgctgct agagttgcc tcggatgtg ctattttaa gtgatattta
180

aatgtaaagt aaccgtatca ttacagtatt gagagttcaa aggctgttgt tcaactacca
240

tttttgaca gcg
253

<210> 59

<211> 288

<212> DNA

<213> Homo sapiens

<400> 59

acggttactc atcgaggac atcgctact actggtcgga gagccaggag cacatccacg
60

ggctggacaa gctgcagctg ggcgcgttca ccatcaccag ctaccgttc accacggagc
120

tgtgaacct caagtccgt aacatatgcc cgccgccttccatgtc cccggccccc
180

cttccgcgcg cgccccaccgc cccttccgcg cgccgcacc gccccttccg cgtgcgcgg
240

SequencesSSCPre-file7August03.ST25.txt
cctgtggttt tcatgcttt tagtcaagcc gccccgcaggc cccccaggc
288

<210> 60
<211> 288
<212> DNA
<213> Homo sapiens

<400> 60
acggttactc atcggaggac atcgtctact actggtcgga gagccaggag cacatccacg
60

ggctggacaa gctgcagctg gcgcagttca ccatcaccag ctaccgcttc accacggagc
120

tgatgaacctt caagtccggt aacatatgcc cgccgcggct tccgcattgtg cccgcggccc
180

cttccgcgcg cgccccaccgc cccttccgcg cgcgccaccg gccccttccg cgtgcgcggc
240

cctgtggttt tcatgcttt tagtcaacgc gccccgcaggc cccccaggc
288

<210> 61
<211> 288
<212> DNA
<213> Homo sapiens

<400> 61
acggttactc atcggaggac atcgtctact actggtcgga gagccaggag cacatccacg
60

ggctggacaa gctgcagctg gcgcagttca ccatcaccag ctaccgcttc accacggagc
120

tgatgaacctt caagtccggt aacatatgcc cgccgcggct tccgcattgtg cccgcggccc
180

cttccgcgcg cgccccaccgc cccttccgcg tgcgccgcg tgggttttc atgctttta
240

gtcaagcgcc cgcaaggcccc cagggcctct ggggatgcag ctgggacg
288

<210> 62
<211> 170
<212> DNA
<213> Homo sapiens

<400> 62
accggtgatg tggcttggtt tagtcataacc ctaaagattg ctcttaagag tgatcttgga

60

SequencesSSCPre-file7August03.ST25.txt

tgcaaatgtt catgacagtt tccttagttat ttttttttat ttttttgtag ttactacatc
120

cagattcctc aagatggatt cctgagcgaa taagctaca agcccttcc
170

<210> 63
<211> 218
<212> PRT
<213> Homo sapiens

<400> 63

Met Gly Arg Leu Leu Ala Leu Val Val Gly Ala Ala Leu Val Ser Ser
1 5 10 15

Ala Cys Gly Gly Cys Val Glu Val Asp Ser Glu Thr Glu Ala Val Tyr
20 25 30

Gly Met Thr Phe Lys Ile Leu Cys Ile Ser Cys Lys Arg Arg Ser Glu
35 40 45

Thr Asn Ala Glu Thr Phe Thr Glu Trp Thr Phe Arg Gln Lys Gly Thr
50 55 60

Glu Glu Phe Val Lys Ile Leu Arg Tyr Glu Asn Glu Val Leu Gln Leu
65 70 75 80

Glu Glu Asp Glu His Phe Glu Gly Arg Val Val Trp Asn Gly Ser Arg
85 90 95

Gly Thr Lys Asp Leu Gln Asp Leu Ser Ile Phe Ile Thr Asn Val Thr
100 105 110

Tyr Asn His Ser Gly Asp Tyr Glu Cys His Val Tyr Arg Leu Leu Phe
115 120 125

Phe Glu Asn Tyr Glu His Asn Thr Ser Val Val Lys Lys Ile His Ile
130 135 140

Glu Val Val Asp Lys Ala Asn Arg Asp Met Ala Ser Ile Val Ser Glu
145 150 155 160

SequencesSSCPre-file7August03.ST25.txt

Ile Met Met Tyr Val Leu Ile Val Val Leu Thr Ile Trp Leu Val Ala
165 170 175

Glu Met Ile Tyr Cys Tyr Lys Lys Ile Ala Ala Ala Thr Glu Thr Ala
180 185 190

Ala Gln Glu Asn Ala Ser Glu Tyr Leu Ala Ile Thr Ser Glu Ser Lys
195 200 205

Glu Asn Cys Thr Gly Val Gln Val Ala Glu
210 215

<210> 64
<211> 2005
<212> PRT
<213> Homo sapiens

<400> 64

Met Ala Gln Ser Val Leu Val Pro Pro Gly Pro Asp Ser Phe Arg Phe
1 5 10 15

Phe Thr Arg Glu Ser Leu Ala Ala Ile Glu Gln Arg Ile Ala Glu Glu
20 25 30

Lys Ala Lys Arg Pro Lys Gln Glu Arg Lys Asp Glu Asp Asp Glu Asn
35 40 45

Gly Pro Lys Pro Asn Ser Asp Leu Glu Ala Gly Lys Ser Leu Pro Phe
50 55 60

Ile Tyr Gly Asp Ile Pro Pro Glu Met Val Ser Val Pro Leu Glu Asp
65 70 75 80

Leu Asp Pro Tyr Tyr Ile Asn Lys Lys Thr Phe Ile Val Leu Asn Lys
85 90 95

Gly Lys Ala Ile Ser Arg Phe Ser Ala Thr Pro Ala Leu Tyr Ile Leu
100 105 110

Thr Pro Phe Asn Pro Ile Arg Lys Leu Ala Ile Lys Ile Leu Val His
115 120 125

SequencesSSCPre-file7August03.ST25.txt

Ser Leu Phe Asn Met Leu Ile Met Cys Thr Ile Leu Thr Asn Cys Val
130 135 140

Phe Met Thr Met Ser Asn Pro Pro Asp Trp Thr Lys Asn Val Glu Tyr
145 150 155 160

Thr Phe Thr Gly Ile Tyr Thr Phe Glu Ser Leu Ile Lys Ile Leu Ala
165 170 175

Arg Gly Phe Cys Leu Glu Asp Phe Thr Phe Leu Arg Asp Pro Trp Asn
180 185 190

Trp Leu Asp Phe Thr Val Ile Thr Phe Ala Tyr Val Thr Glu Phe Val
195 200 205

Asp Leu Gly Asn Val Ser Ala Leu Arg Thr Phe Arg Val Leu Gln Ala
210 215 220

Leu Lys Thr Ile Ser Val Ile Pro Gly Leu Lys Thr Ile Val Gly Ala
225 230 235 240

Leu Ile Gln Ser Val Lys Lys Leu Ser Asp Val Met Ile Leu Thr Val
245 250 255

Phe Cys Leu Ser Val Phe Ala Leu Ile Gly Leu Gln Leu Phe Met Gly
260 265 270

Asn Leu Arg Asn Lys Cys Leu Gln Trp Pro Pro Asp Asn Ser Ser Phe
275 280 285

Glu Ile Asn Ile Thr Ser Phe Phe Asn Asn Ser Leu Asp Gly Asn Gly
290 295 300

Thr Thr Phe Asn Arg Thr Val Ser Ile Phe Asn Trp Asp Glu Tyr Ile
305 310 315 320

Glu Asp Lys Ser His Phe Tyr Phe Leu Glu Gly Gln Asn Asp Ala Leu
325 330 335

Leu Cys Gly Asn Ser Ser Asp Ala Gly Gln Cys Pro Glu Gly Tyr Ile
340 345 350

SequencesSSCPRe-file7August03.ST25.txt

Cys Val Lys Ala Gly Arg Asn Pro Asn Tyr Gly Tyr Thr Ser Phe Asp
355 360 365

Thr Phe Ser Trp Ala Phe Leu Ser Leu Phe Arg Leu Met Thr Gln Asp
370 375 380

Phe Trp Glu Asn Leu Tyr Gln Leu Thr Leu Arg Ala Ala Gly Lys Thr
385 390 395 400

Tyr Met Ile Phe Phe Val Leu Val Ile Phe Leu Gly Ser Phe Tyr Leu
405 410 415

Ile Asn Leu Ile Leu Ala Val Val Ala Met Ala Tyr Glu Glu Gln Asn
420 425 430

Gln Ala Thr Leu Glu Glu Ala Glu Gln Lys Glu Ala Glu Phe Gln Gln
435 440 445

Met Leu Glu Gln Leu Lys Lys Gln Gln Glu Ala Gln Ala Ala Ala
450 455 460

Ala Ala Ala Ser Ala Glu Ser Arg Asp Phe Ser Gly Ala Gly Gly Ile
465 470 475 480

Gly Val Phe Ser Glu Ser Ser Ser Val Ala Ser Lys Leu Ser Ser Lys
485 490 495

Ser Glu Lys Glu Leu Lys Asn Arg Arg Lys Lys Lys Lys Gln Lys Glu
500 505 510

Gln Ser Gly Glu Glu Glu Lys Asn Asp Arg Val Leu Lys Ser Glu Ser
515 520 525

Glu Asp Ser Ile Arg Arg Lys Gly Phe Arg Phe Ser Leu Glu Gly Ser
530 535 540

Arg Leu Thr Tyr Glu Lys Arg Phe Ser Ser Pro His Gln Ser Leu Leu
545 550 555 560

Ser Ile Arg Gly Ser Leu Phe Ser Pro Arg Arg Asn Ser Arg Ala Ser

SequencesSSCPre-file7August03.ST25.txt
565 570

575

Leu Phe Ser Phe Arg Gly Arg Ala Lys Asp Ile Gly Ser Glu Asn Asp
580 585 590

Phe Ala Asp Asp Glu His Ser Thr Phe Glu Asp Asn Asp Ser Arg Arg
595 600 605

Asp Ser Leu Phe Val Pro His Arg His Gly Glu Arg Arg His Ser Asn
610 615 620

Val Ser Gln Ala Ser Arg Ala Ser Arg Val Leu Pro Ile Leu Pro Met
625 630 635 640

Asn Gly Lys Met His Ser Ala Val Asp Cys Asn Gly Val Val Ser Leu
645 650 655

Val Gly Gly Pro Ser Thr Leu Thr Ser Ala Gly Gln Leu Leu Pro Glu
660 665 670

Gly Thr Thr Glu Thr Glu Ile Arg Lys Arg Arg Ser Ser Ser Tyr
675 680 685

His Val Ser Met Asp Leu Leu Glu Asp Pro Thr Ser Arg Gln Arg Ala
690 695 700

Met Ser Ile Ala Ser Ile Leu Thr Asn Thr Met Glu Glu Leu Glu Glu
705 710 715 720

Ser Arg Gln Lys Cys Pro Pro Cys Trp Tyr Lys Phe Ala Asn Met Cys
725 730 735

Leu Ile Trp Asp Cys Cys Lys Pro Trp Leu Lys Val Lys His Leu Val
740 745 750

Asn Leu Val Val Met Asp Pro Phe Val Asp Leu Ala Ile Thr Ile Cys
755 760 765

Ile Val Leu Asn Thr Leu Phe Met Ala Met Glu His Tyr Pro Met Thr
770 775 780

SequencesSSCPRe-file7August03.ST25.txt

Glu Gln Phe Ser Ser Val Leu Ser Val Gly Asn Leu Val Phe Thr Gly
785 790 795 800

Ile Phe Thr Ala Glu Met Phe Leu Lys Ile Ile Ala Met Asp Pro Tyr
805 810 815

Tyr Tyr Phe Gln Glu Gly Trp Asn Ile Phe Asp Gly Phe Ile Val Ser
820 825 830

Leu Ser Leu Met Glu Leu Gly Leu Ala Asn Val Glu Gly Leu Ser Val
835 840 845

Leu Arg Ser Phe Arg Leu Leu Arg Val Phe Lys Leu Ala Lys Ser Trp
850 855 860

Pro Thr Leu Asn Met Leu Ile Lys Ile Ile Gly Asn Ser Val Gly Ala
865 870 875 880

Leu Gly Asn Leu Thr Leu Val Leu Ala Ile Ile Val Phe Ile Phe Ala
885 890 895

Val Val Gly Met Gln Leu Phe Gly Lys Ser Tyr Lys Glu Cys Val Cys
900 905 910

Lys Ile Ser Asn Asp Cys Glu Leu Pro Arg Trp His Met His Asp Phe
915 920 925

Phe His Ser Phe Leu Ile Val Phe Arg Val Leu Cys Gly Glu Trp Ile
930 935 940

Glu Thr Met Trp Asp Cys Met Glu Val Ala Gly Gln Thr Met Cys Leu
945 950 955 960

Thr Val Phe Met Met Val Met Val Ile Gly Asn Leu Val Val Leu Asn
965 970 975

Leu Phe Leu Ala Leu Leu Ser Ser Phe Ser Ser Asp Asn Leu Ala
980 985 990

Ala Thr Asp Asp Asp Asn Glu Met Asn Asn Leu Gln Ile Ala Val Gly
995 1000 1005

SequencesSSCPre-file7August03.ST25.txt

Arg Met Gln Lys Gly Ile Asp Phe Val Lys Arg Lys Ile Arg Glu
1010 1015 1020

Phe Ile Gln Lys Ala Phe Val Arg Lys Gln Lys Ala Leu Asp Glu
1025 1030 1035

Ile Lys Pro Leu Glu Asp Leu Asn Asn Lys Lys Asp Ser Cys Ile
1040 1045 1050

Ser Asn His Thr Thr Ile Glu Ile Gly Lys Asp Leu Asn Tyr Leu
1055 1060 1065

Lys Asp Gly Asn Gly Thr Thr Ser Gly Ile Gly Ser Ser Val Glu
1070 1075 1080

Lys Tyr Val Val Asp Glu Ser Asp Tyr Met Ser Phe Ile Asn Asn
1085 1090 1095

Pro Ser Leu Thr Val Thr Val Pro Ile Ala Val Gly Glu Ser Asp
1100 1105 1110

Phe Glu Asn Leu Asn Thr Glu Glu Phe Ser Ser Glu Ser Asp Met
1115 1120 1125

Glu Glu Ser Lys Glu Lys Leu Asn Ala Thr Ser Ser Ser Glu Gly
1130 1135 1140

Ser Thr Val Asp Ile Gly Ala Pro Ala Glu Gly Glu Gln Pro Glu
1145 1150 1155

Val Glu Pro Glu Glu Ser Leu Glu Pro Glu Ala Cys Phe Thr Glu
1160 1165 1170

Asp Cys Val Arg Lys Phe Lys Cys Cys Gln Ile Ser Ile Glu Glu
1175 1180 1185

Gly Lys Gly Lys Leu Trp Trp Asn Leu Arg Lys Thr Cys Tyr Lys
1190 1195 1200

Ile Val Glu His Asn Trp Phe Glu Thr Phe Ile Val Phe Met Ile
1205 1210 1215

SequencesSSCPRe-file7August03.ST25.txt

Leu Leu Ser Ser Gly Ala Leu Ala Phe Glu Asp Ile Tyr Ile Glu
1220 1225 1230

Gln Arg Lys Thr Ile Lys Thr Met Leu Glu Tyr Ala Asp Lys Val
1235 1240 1245

Phe Thr Tyr Ile Phe Ile Leu Glu Met Leu Leu Lys Trp Val Ala
1250 1255 1260

Tyr Gly Phe Gln Val Tyr Phe Thr Asn Ala Trp Cys Trp Leu Asp
1265 1270 1275

Phe Leu Ile Val Asp Val Ser Leu Val Ser Leu Thr Ala Asn Ala
1280 1285 1290

Leu Gly Tyr Ser Glu Leu Gly Ala Ile Lys Ser Leu Arg Thr Leu
1295 1300 1305

Arg Ala Leu Arg Pro Leu Arg Ala Leu Ser Arg Phe Glu Gly Met
1310 1315 1320

Arg Val Val Val Asn Ala Leu Leu Gly Ala Ile Pro Ser Ile Met
1325 1330 1335

Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu Ile Phe Ser Ile
1340 1345 1350

Met Gly Val Asn Leu Phe Ala Gly Lys Phe Tyr His Cys Ile Asn
1355 1360 1365

Tyr Thr Thr Gly Glu Met Phe Asp Val Ser Val Val Asn Asn Tyr
1370 1375 1380

Ser Glu Cys Lys Ala Leu Ile Glu Ser Asn Gln Thr Ala Arg Trp
1385 1390 1395

Lys Asn Val Lys Val Asn Phe Asp Asn Val Gly Leu Gly Tyr Leu
1400 1405 1410

Ser Leu Leu Gln Val Ala Thr Phe Lys Gly Trp Met Asp Ile Met

SequencesSSCPRe-file7August03.ST25.txt
1415 1420 1425

Tyr Ala Ala Val Asp Ser Arg Asn Val Glu Leu Gln Pro Lys Tyr
1430 1435 1440

Glu Asp Asn Leu Tyr Met Tyr Leu Tyr Phe Val Ile Phe Ile Ile
1445 1450 1455

Phe Gly Ser Phe Phe Thr Leu Asn Leu Phe Ile Gly Val Ile Ile
1460 1465 1470

Asp Asn Phe Asn Gln Gln Lys Lys Lys Phe Gly Gly Gln Asp Ile
1475 1480 1485

Phe Met Thr Glu Glu Gln Lys Lys Tyr Tyr Asn Ala Met Lys Lys
1490 1495 1500

Leu Gly Ser Lys Lys Pro Gln Lys Pro Ile Pro Arg Pro Ala Asn
1505 1510 1515

Lys Phe Gln Gly Met Val Phe Asp Phe Val Thr Lys Gln Val Phe
1520 1525 1530

Asp Ile Ser Ile Met Ile Leu Ile Cys Leu Asn Met Val Thr Met
1535 1540 1545

Met Val Glu Thr Asp Asp Gln Ser Gln Glu Met Thr Asn Ile Leu
1550 1555 1560

Tyr Trp Ile Asn Leu Val Phe Ile Val Leu Phe Thr Gly Glu Cys
1565 1570 1575

Val Leu Lys Leu Ile Ser Leu Arg Tyr Tyr Tyr Phe Thr Ile Gly
1580 1585 1590

Trp Asn Ile Phe Asp Phe Val Val Val Ile Leu Ser Ile Val Gly
1595 1600 1605

Met Phe Leu Ala Glu Leu Ile Glu Lys Tyr Phe Val Ser Pro Thr
1610 1615 1620

SequencesSSCPRe-file7August03.ST25.txt

Leu Phe Arg Val Ile Arg Leu Ala Arg Ile Gly Arg Ile Leu Arg
1625 1630 1635

Leu Ile Lys Gly Ala Lys Gly Ile Arg Thr Leu Leu Phe Ala Leu
1640 1645 1650

Met Met Ser Leu Pro Ala Leu Phe Asn Ile Gly Leu Leu Leu Phe
1655 1660 1665

Leu Val Met Phe Ile Tyr Ala Ile Phe Gly Met Ser Asn Phe Ala
1670 1675 1680

Tyr Val Lys Arg Glu Val Gly Ile Asp Asp Met Phe Asn Phe Glu
1685 1690 1695

Thr Phe Gly Asn Ser Met Ile Cys Leu Phe Gln Ile Thr Thr Ser
1700 1705 1710

Ala Gly Trp Asp Gly Leu Leu Ala Pro Ile Leu Asn Ser Gly Pro
1715 1720 1725

Pro Asp Cys Asp Pro Asp Lys Asp His Pro Gly Ser Ser Val Lys
1730 1735 1740

Gly Asp Cys Gly Asn Pro Ser Val Gly Ile Phe Phe Phe Val Ser
1745 1750 1755

Tyr Ile Ile Ile Ser Phe Leu Val Val Leu Asn Met Tyr Ile Ala
1760 1765 1770

Val Ile Leu Glu Asn Phe Ser Val Ala Thr Glu Glu Ser Ala Glu
1775 1780 1785

Pro Leu Ser Glu Asp Asp Phe Glu Met Phe Tyr Glu Val Trp Glu
1790 1795 1800

Lys Phe Asp Pro Asp Ala Thr Gln Phe Ile Glu Phe Ala Lys Leu
1805 1810 1815

Ser Asp Phe Ala Asp Ala Leu Asp Pro Pro Leu Leu Ile Ala Lys
1820 1825 1830

SequencesSSCPRe-file7August03.ST25.txt

Pro Asn Lys Val Gln Leu Ile Ala Met Asp Leu Pro Met Val Ser
1835 1840 1845

Gly Asp Arg Ile His Cys Leu Asp Ile Leu Phe Ala Phe Thr Lys
1850 1855 1860

Arg Val Leu Gly Glu Ser Gly Glu Met Asp Ala Leu Arg Ile Gln
1865 1870 1875

Met Glu Glu Arg Phe Met Ala Ser Asn Pro Ser Lys Val Ser Tyr
1880 1885 1890

Glu Pro Ile Thr Thr Leu Lys Arg Lys Gln Glu Glu Val Ser
1895 1900 1905

Ala Ile Ile Ile Gln Arg Ala Tyr Arg Arg Tyr Leu Leu Lys Gln
1910 1915 1920

Lys Val Lys Lys Val Ser Ser Ile Tyr Lys Lys Asp Lys Gly Lys
1925 1930 1935

Glu Cys Asp Gly Thr Pro Ile Lys Glu Asp Thr Leu Ile Asp Lys
1940 1945 1950

Leu Asn Glu Asn Ser Thr Pro Glu Lys Thr Asp Met Thr Pro Ser
1955 1960 1965

Thr Thr Ser Pro Pro Ser Tyr Asp Ser Val Thr Lys Pro Glu Lys
1970 1975 1980

Glu Lys Phe Glu Lys Asp Lys Ser Glu Lys Glu Asp Lys Gly Lys
1985 1990 1995

Asp Ile Arg Glu Ser Lys Lys
2000 2005

<210> 65
<211> 2005
<212> PRT
<213> Homo sapiens

<400> 65

SequencesSSCPRe-file7August03.ST25.txt

Met Ala Gln Ser Val Leu Val Pro Pro Gly Pro Asp Ser Phe Arg Phe
1 5 10 15

Phe Thr Arg Glu Ser Leu Ala Ala Ile Glu Gln Arg Ile Ala Glu Glu
20 25 30

Lys Ala Lys Arg Pro Lys Gln Glu Arg Lys Asp Glu Asp Asp Glu Asn
35 40 45

Gly Pro Lys Pro Asn Ser Asp Leu Glu Ala Gly Lys Ser Leu Pro Phe
50 55 60

Ile Tyr Gly Asp Ile Pro Pro Glu Met Val Ser Val Pro Leu Glu Asp
65 70 75 80

Leu Asp Pro Tyr Tyr Ile Asn Lys Lys Thr Phe Ile Val Leu Asn Lys
85 90 95

Gly Lys Ala Ile Ser Arg Phe Ser Ala Thr Pro Ala Leu Tyr Ile Leu
100 105 110

Thr Pro Phe Asn Pro Ile Arg Lys Leu Ala Ile Lys Ile Leu Val His
115 120 125

Ser Leu Phe Asn Met Leu Ile Met Cys Thr Ile Leu Thr Asn Cys Val
130 135 140

Phe Met Thr Met Ser Asn Pro Pro Asp Trp Thr Lys Asn Val Glu Tyr
145 150 155 160

Thr Phe Thr Gly Ile Tyr Thr Phe Glu Ser Leu Ile Lys Ile Leu Ala
165 170 175

Arg Gly Phe Cys Leu Glu Asp Phe Thr Phe Leu Arg Asp Pro Trp Asn
180 185 190

Trp Leu Asp Phe Thr Val Ile Thr Phe Ala Tyr Val Thr Glu Phe Val
195 200 205

Asp Leu Gly Asn Val Ser Ala Leu Arg Thr Phe Arg Val Leu Arg Ala
210 215 220

SequencesSSCPRe-file7August03.ST25.txt

Leu Lys Thr Ile Ser Val Ile Pro Gly Leu Lys Thr Ile Val Gly Ala
225 230 235 240

Leu Ile Gln Ser Val Lys Lys Leu Ser Asp Val Met Ile Leu Thr Val
245 250 255

Phe Cys Leu Ser Val Phe Ala Leu Ile Gly Leu Gln Leu Phe Met Gly
260 265 270

Asn Leu Arg Asn Lys Cys Leu Gln Trp Pro Pro Asp Asn Ser Ser Phe
275 280 285

Glu Ile Asn Ile Thr Ser Phe Phe Asn Asn Ser Leu Asp Gly Asn Gly
290 295 300

Thr Thr Phe Asn Arg Thr Val Ser Ile Phe Asn Trp Asp Glu Tyr Ile
305 310 315 320

Glu Asp Lys Ser His Phe Tyr Phe Leu Glu Gly Gln Asn Asp Ala Leu
325 330 335

Leu Cys Gly Asn Ser Ser Asp Ala Gly Gln Cys Pro Glu Gly Tyr Ile
340 345 350

Cys Val Lys Ala Gly Arg Asn Pro Asn Tyr Gly Tyr Thr Ser Phe Asp
355 360 365

Thr Phe Ser Trp Ala Phe Leu Ser Leu Phe Arg Leu Met Thr Gln Asp
370 375 380

Phe Trp Glu Asn Leu Tyr Gln Leu Thr Leu Arg Ala Ala Gly Lys Thr
385 390 395 400

Tyr Met Ile Phe Phe Val Leu Val Ile Phe Leu Gly Ser Phe Tyr Leu
405 410 415

Ile Asn Leu Ile Leu Ala Val Val Ala Met Ala Tyr Glu Glu Gln Asn
420 425 430

Gln Ala Thr Leu Glu Glu Ala Glu Gln Lys Glu Ala Glu Phe Gln Gln

SequencesSSCPre-file7August03.ST25.txt

435

440

445

Met Leu Glu Gln Leu Lys Lys Gln Gln Glu Ala Gln Ala Ala Ala
450 455 460

Ala Ala Ala Ser Ala Glu Ser Arg Asp Phe Ser Gly Ala Gly Gly Ile
465 470 475 480

Gly Val Phe Ser Glu Ser Ser Ser Val Ala Ser Lys Leu Ser Ser Lys
485 490 495

Ser Glu Lys Glu Leu Lys Asn Arg Arg Lys Lys Lys Lys Gln Lys Glu
500 505 510

Gln Ser Gly Glu Glu Glu Lys Asn Asp Arg Val Leu Lys Ser Glu Ser
515 520 525

Glu Asp Ser Ile Arg Arg Lys Gly Phe Arg Phe Ser Leu Glu Gly Ser
530 535 540

Arg Leu Thr Tyr Glu Lys Arg Phe Ser Ser Pro His Gln Ser Leu Leu
545 550 555 560

Ser Ile Arg Gly Ser Leu Phe Ser Pro Arg Arg Asn Ser Arg Ala Ser
565 570 575

Leu Phe Ser Phe Arg Gly Arg Ala Lys Asp Ile Gly Ser Glu Asn Asp
580 585 590

Phe Ala Asp Asp Glu His Ser Thr Phe Glu Asp Asn Asp Ser Arg Arg
595 600 605

Asp Ser Leu Phe Val Pro His Arg His Gly Glu Arg Arg His Ser Asn
610 615 620

Val Ser Gln Ala Ser Arg Ala Ser Arg Val Leu Pro Ile Leu Pro Met
625 630 635 640

Asn Gly Lys Met His Ser Ala Val Asp Cys Asn Gly Val Val Ser Leu
645 650 655

SequencesSSCPRe-file7August03.ST25.txt
Val Gly Gly Pro Ser Thr Leu Thr Ser Ala Gly Gln Leu Leu Pro Glu
660 665 670

Gly Thr Thr Thr Glu Thr Glu Ile Arg Lys Arg Arg Ser Ser Ser Tyr
675 680 685

His Val Ser Met Asp Leu Leu Glu Asp Pro Thr Ser Arg Gln Arg Ala
690 695 700

Met Ser Ile Ala Ser Ile Leu Thr Asn Thr Met Glu Glu Leu Glu Glu
705 710 715 720

Ser Arg Gln Lys Cys Pro Pro Cys Trp Tyr Lys Phe Ala Asn Met Cys
725 730 735

Leu Ile Trp Asp Cys Cys Lys Pro Trp Leu Lys Val Lys His Leu Val
740 745 750

Asn Leu Val Val Met Asp Pro Phe Val Asp Leu Ala Ile Thr Ile Cys
755 760 765

Ile Val Leu Asn Thr Leu Phe Met Ala Met Glu His Tyr Pro Met Thr
770 775 780

Glu Gln Phe Ser Ser Val Leu Ser Val Gly Asn Leu Val Phe Thr Gly
785 790 795 800

Ile Phe Thr Ala Glu Met Phe Leu Lys Ile Ile Ala Met Asp Pro Tyr
805 810 815

Tyr Tyr Phe Gln Glu Gly Trp Asn Ile Phe Asp Gly Phe Ile Val Ser
820 825 830

Leu Ser Leu Met Glu Leu Gly Leu Ala Asn Val Glu Gly Leu Ser Val
835 840 845

Leu Arg Ser Phe Arg Leu Leu Arg Val Phe Lys Leu Ala Lys Ser Trp
850 855 860

Pro Thr Leu Asn Met Leu Ile Lys Ile Ile Gly Asn Ser Val Gly Ala
865 870 875 880

SequencesSSCPre-file7August03.ST25.txt

Leu Gly Asn Leu Thr Leu Val Leu Ala Ile Ile Ile Phe Ile Phe Ala
885 890 895

Val Val Gly Met Gln Leu Phe Gly Lys Ser Tyr Lys Glu Cys Val Cys
900 905 910

Lys Ile Ser Asn Asp Cys Glu Leu Pro Arg Trp His Met His Asp Phe
915 920 925

Phe His Ser Phe Leu Ile Val Phe Arg Val Leu Cys Gly Glu Trp Ile
930 935 940

Glu Thr Met Trp Asp Cys Met Glu Val Ala Gly Gln Thr Met Cys Leu
945 950 955 960

Thr Val Phe Met Met Val Met Val Ile Gly Asn Leu Val Val Leu Asn
965 970 975

Leu Phe Leu Ala Leu Leu Leu Ser Ser Phe Ser Ser Asp Asn Leu Ala
980 985 990

Ala Thr Asp Asp Asp Asn Glu Met Asn Asn Leu Gln Ile Ala Val Gly
995 1000 1005

Arg Met Gln Lys Gly Ile Asp Phe Val Lys Arg Lys Ile Arg Glu
1010 1015 1020

Phe Ile Gln Lys Ala Phe Val Arg Lys Gln Lys Ala Leu Asp Glu
1025 1030 1035

Ile Lys Pro Leu Glu Asp Leu Asn Asn Lys Lys Asp Ser Cys Ile
1040 1045 1050

Ser Asn His Thr Thr Ile Glu Ile Gly Lys Asp Leu Asn Tyr Leu
1055 1060 1065

Lys Asp Gly Asn Gly Thr Thr Ser Gly Ile Gly Ser Ser Val Glu
1070 1075 1080

Lys Tyr Val Val Asp Glu Ser Asp Tyr Met Ser Phe Ile Asn Asn
1085 1090 1095

SequencesSSCPre-file7August03.ST25.txt

Pro Ser Leu Thr Val Thr Val Pro Ile Ala Val Gly Glu Ser Asp
1100 1105 1110

Phe Glu Asn Leu Asn Thr Glu Glu Phe Ser Ser Glu Ser Asp Met
1115 1120 1125

Glu Glu Ser Lys Glu Lys Leu Asn Ala Thr Ser Ser Ser Glu Gly
1130 1135 1140

Ser Thr Val Asp Ile Gly Ala Pro Ala Glu Gly Glu Gln Pro Glu
1145 1150 1155

Val Glu Pro Glu Glu Ser Leu Glu Pro Glu Ala Cys Phe Thr Glu
1160 1165 1170

Asp Cys Val Arg Lys Phe Lys Cys Cys Gln Ile Ser Ile Glu Glu
1175 1180 1185

Gly Lys Gly Lys Leu Trp Trp Asn Leu Arg Lys Thr Cys Tyr Lys
1190 1195 1200

Ile Val Glu His Asn Trp Phe Glu Thr Phe Ile Val Phe Met Ile
1205 1210 1215

Leu Leu Ser Ser Gly Ala Leu Ala Phe Glu Asp Ile Tyr Ile Glu
1220 1225 1230

Gln Arg Lys Thr Ile Lys Thr Met Leu Glu Tyr Ala Asp Lys Val
1235 1240 1245

Phe Thr Tyr Ile Phe Ile Leu Glu Met Leu Leu Lys Trp Val Ala
1250 1255 1260

Tyr Gly Phe Gln Val Tyr Phe Thr Asn Ala Trp Cys Trp Leu Asp
1265 1270 1275

Phe Leu Ile Val Asp Val Ser Leu Val Ser Leu Thr Ala Asn Ala
1280 1285 1290

Leu Gly Tyr Ser Glu Leu Gly Ala Ile Lys Ser Leu Arg Thr Leu
Page 166

1295

SequencesSSCPre-file7August03.ST25.txt
1300 1305

Arg Ala Leu Arg Pro Leu Arg Ala Leu Ser Arg Phe Glu Gly Met
1310 1315 1320

Arg Val Val Val Asn Ala Leu Leu Gly Ala Ile Pro Ser Ile Met
1325 1330 1335

Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu Ile Phe Ser Ile
1340 1345 1350

Met Gly Val Asn Leu Phe Ala Gly Lys Phe Tyr His Cys Ile Asn
1355 1360 1365

Tyr Thr Thr Gly Glu Met Phe Asp Val Ser Val Val Asn Asn Tyr
1370 1375 1380

Ser Glu Cys Lys Ala Leu Ile Glu Ser Asn Gln Thr Ala Arg Trp
1385 1390 1395

Lys Asn Val Lys Val Asn Phe Asp Asn Val Gly Leu Gly Tyr Leu
1400 1405 1410

Ser Leu Leu Gln Val Ala Thr Phe Lys Gly Trp Met Asp Ile Met
1415 1420 1425

Tyr Ala Ala Val Asp Ser Arg Asn Val Glu Leu Gln Pro Lys Tyr
1430 1435 1440

Glu Asp Asn Leu Tyr Met Tyr Leu Tyr Phe Val Ile Phe Ile Ile
1445 1450 1455

Phe Gly Ser Phe Phe Thr Leu Asn Leu Phe Ile Gly Val Ile Ile
1460 1465 1470

Asp Asn Phe Asn Gln Gln Lys Lys Lys Phe Gly Gly Gln Asp Ile
1475 1480 1485

Phe Met Thr Glu Glu Gln Lys Lys Tyr Tyr Asn Ala Met Lys Lys
1490 1495 1500

SequencesSSCPRe-file7August03.ST25.txt

Leu Gly Ser Lys Lys Pro Gln Lys Pro Ile Pro Arg Pro Ala Asn
1505 1510 1515

Lys Phe Gln Gly Met Val Phe Asp Phe Val Thr Lys Gln Val Phe
1520 1525 1530

Asp Ile Ser Ile Met Ile Leu Ile Cys Leu Asn Met Val Thr Met
1535 1540 1545

Met Val Glu Thr Asp Asp Gln Ser Gln Glu Met Thr Asn Ile Leu
1550 1555 1560

Tyr Trp Ile Asn Leu Val Phe Ile Val Leu Phe Thr Gly Glu Cys
1565 1570 1575

Val Leu Lys Leu Ile Ser Leu Arg Tyr Tyr Tyr Phe Thr Ile Gly
1580 1585 1590

Trp Asn Ile Phe Asp Phe Val Val Val Ile Leu Ser Ile Val Gly
1595 1600 1605

Met Phe Leu Ala Glu Leu Ile Glu Lys Tyr Phe Val Ser Pro Thr
1610 1615 1620

Leu Phe Arg Val Ile Arg Leu Ala Arg Ile Gly Arg Ile Leu Arg
1625 1630 1635

Leu Ile Lys Gly Ala Lys Gly Ile Arg Thr Leu Leu Phe Ala Leu
1640 1645 1650

Met Met Ser Leu Pro Ala Leu Phe Asn Ile Gly Leu Leu Leu Phe
1655 1660 1665

Leu Val Met Phe Ile Tyr Ala Ile Phe Gly Met Ser Asn Phe Ala
1670 1675 1680

Tyr Val Lys Arg Glu Val Gly Ile Asp Asp Met Phe Asn Phe Glu
1685 1690 1695

Thr Phe Gly Asn Ser Met Ile Cys Leu Phe Gln Ile Thr Thr Ser
1700 1705 1710

SequencesSSCPRe-file7August03.ST25.txt

Ala Gly Trp Asp Gly Leu Leu Ala Pro Ile Leu Asn Ser Gly Pro
1715 1720 1725

Pro Asp Cys Asp Pro Asp Lys Asp His Pro Gly Ser Ser Val Lys
1730 1735 1740

Gly Asp Cys Gly Asn Pro Ser Val Gly Ile Phe Phe Phe Val Ser
1745 1750 1755

Tyr Ile Ile Ile Ser Phe Leu Val Val Leu Asn Met Tyr Ile Ala
1760 1765 1770

Val Ile Leu Glu Asn Phe Ser Val Ala Thr Glu Glu Ser Ala Glu
1775 1780 1785

Pro Leu Ser Glu Asp Asp Phe Glu Met Phe Tyr Glu Val Trp Glu
1790 1795 1800

Lys Phe Asp Pro Asp Ala Thr Gln Phe Ile Glu Phe Ala Lys Leu
1805 1810 1815

Ser Asp Phe Ala Asp Ala Leu Asp Pro Pro Leu Leu Ile Ala Lys
1820 1825 1830

Pro Asn Lys Val Gln Leu Ile Ala Met Asp Leu Pro Met Val Ser
1835 1840 1845

Gly Asp Arg Ile His Cys Leu Asp Ile Leu Phe Ala Phe Thr Lys
1850 1855 1860

Arg Val Leu Gly Glu Ser Gly Glu Met Asp Ala Leu Arg Ile Gln
1865 1870 1875

Met Glu Glu Arg Phe Met Ala Ser Asn Pro Ser Lys Val Ser Tyr
1880 1885 1890

Glu Pro Ile Thr Thr Thr Leu Lys Arg Lys Gln Glu Glu Val Ser
1895 1900 1905

Ala Ile Ile Ile Gln Arg Ala Tyr Arg Arg Tyr Leu Leu Lys Gln
1910 1915 1920

SequencesSSCPRe-file7August03.ST25.txt

Lys Val Lys Lys Val Ser Ser Ile Tyr Lys Lys Asp Lys Gly Lys
1925 1930 1935

Glu Cys Asp Gly Thr Pro Ile Lys Glu Asp Thr Leu Ile Asp Lys
1940 1945 1950

Leu Asn Glu Asn Ser Thr Pro Glu Lys Thr Asp Met Thr Pro Ser
1955 1960 1965

Thr Thr Ser Pro Pro Ser Tyr Asp Ser Val Thr Lys Pro Glu Lys
1970 1975 1980

Glu Lys Phe Glu Lys Asp Lys Ser Glu Lys Glu Asp Lys Gly Lys
1985 1990 1995

Asp Ile Arg Glu Ser Lys Lys
2000 2005

<210> 66
<211> 2005
<212> PRT
<213> Homo sapiens

<400> 66

Met Ala Gln Ser Val Leu Val Pro Pro Gly Pro Asp Ser Phe Arg Phe
1 5 10 15

Phe Thr Arg Glu Ser Leu Ala Ala Ile Glu Gln Arg Ile Ala Glu Glu
20 25 30

Lys Ala Lys Arg Pro Lys Gln Glu Arg Lys Asp Glu Asp Asp Glu Asn
35 40 45

Gly Pro Lys Pro Asn Ser Asp Leu Glu Ala Gly Lys Ser Leu Pro Phe
50 55 60

Ile Tyr Gly Asp Ile Pro Pro Glu Met Val Ser Val Pro Leu Glu Asp
65 70 75 80

Leu Asp Pro Tyr Tyr Ile Asn Lys Lys Thr Phe Ile Val Leu Asn Lys
85 90 95

SequencesSSCPRe-file7August03.ST25.txt

Gly Lys Ala Ile Ser Arg Phe Ser Ala Thr Pro Ala Leu Tyr Ile Leu
100 105 110

Thr Pro Phe Asn Pro Ile Arg Lys Leu Ala Ile Lys Ile Leu Val His
115 120 125

Ser Leu Phe Asn Met Leu Ile Met Cys Thr Ile Leu Thr Asn Cys Val
130 135 140

Phe Met Thr Met Ser Asn Pro Pro Asp Trp Thr Lys Asn Val Glu Tyr
145 150 155 160

Thr Phe Thr Gly Ile Tyr Thr Phe Glu Ser Leu Ile Lys Ile Leu Ala
165 170 175

Arg Gly Phe Cys Leu Glu Asp Phe Thr Phe Leu Arg Asp Pro Trp Asn
180 185 190

Trp Leu Asp Phe Thr Val Ile Thr Phe Ala Tyr Val Thr Glu Phe Val
195 200 205

Asp Leu Gly Asn Val Ser Ala Leu Arg Thr Phe Arg Val Leu Arg Ala
210 215 220

Leu Lys Thr Ile Ser Val Ile Pro Gly Leu Lys Thr Ile Val Gly Ala
225 230 235 240

Leu Ile Gln Ser Val Lys Lys Leu Ser Asp Val Met Ile Leu Thr Val
245 250 255

Phe Cys Leu Ser Val Phe Ala Leu Ile Gly Leu Gln Leu Phe Met Gly
260 265 270

Asn Leu Arg Asn Lys Cys Leu Gln Trp Pro Pro Asp Asn Ser Ser Phe
275 280 285

Glu Ile Asn Ile Thr Ser Phe Phe Asn Asn Ser Leu Asp Gly Asn Gly
290 295 300

Thr Thr Phe Asn Arg Thr Val Ser Ile Phe Asn Trp Asp Glu Tyr Ile

SequencesSSCPRe-file7August03.ST25.txt

305 310 315 320

Glu Asp Lys Ser His Phe Tyr Phe Leu Glu Gly Gln Asn Asp Ala Leu
 325 330 335

Leu Cys Gly Asn Ser Asp Ala Gly Gln Cys Pro Glu Gly Tyr Ile
340 345 350

Cys Val Lys Ala Gly Arg Asn Pro Asn Tyr Gly Tyr Thr Ser Phe Asp
 355 360 365

Thr Phe Ser Trp Ala Phe Leu Ser Leu Phe Arg Leu Met Thr Gln Asp
370 375 380

Phe Trp Glu Asn Leu Tyr Gln Leu Thr Leu Arg Ala Ala Gly Lys Thr
 385 390 395 400

Tyr Met Ile Phe Phe Val Leu Val Ile Phe Leu Gly Ser Phe Tyr Leu
405 410 415

Ile Asn Leu Ile Leu Ala Val Val Ala Met Ala Tyr Glu Glu Gln Asn
420 425 430

Gln Ala Thr Leu Glu Glu Ala Glu Gln Lys Glu Ala Glu Phe Gln Gln
435 440 445

Met Leu Glu Gln Leu Lys Lys Gln Gln Glu Glu Ala Gln Ala Ala Ala
450 455 . 460

Ala Ala Ala Ser Ala Glu Ser Arg Asp Phe Ser Gly Ala Gly Gly Ile
465 470 475 480

Gly Val Phe Ser Glu Ser Ser Ser Val Ala Ser Lys Leu Ser Ser Lys
485 490 495

Ser Glu Lys Glu Leu Lys Asn Arg Arg Lys Lys Lys Lys Gln Lys Glu
500 505 510

Gln Ser Gly Glu Glu Glu Lys Asn Asp Arg Val Leu Lys Ser Glu Ser
515 520 525

SequencesSSCPRe-file7August03.ST25.txt

Glu Asp Ser Ile Arg Arg Lys Gly Phe Arg Phe Ser Leu Glu Gly Ser
530 535 540

Arg Leu Thr Tyr Glu Lys Arg Phe Ser Ser Pro His Gln Ser Leu Leu
545 550 555 560

Ser Ile Arg Gly Ser Leu Phe Ser Pro Arg Arg Asn Ser Arg Ala Ser
565 570 575

Leu Phe Ser Phe Arg Gly Arg Ala Lys Asp Ile Gly Ser Glu Asn Asp
580 585 590

Phe Ala Asp Asp Glu His Ser Thr Phe Glu Asp Asn Asp Ser Arg Arg
595 600 605

Asp Ser Leu Phe Val Pro His Arg His Gly Glu Arg Arg His Ser Asn
610 615 620

Val Ser Gln Ala Ser Arg Ala Ser Arg Val Leu Pro Ile Leu Pro Met
625 630 635 640

Asn Gly Lys Met His Ser Ala Val Asp Cys Asn Gly Val Val Ser Leu
645 650 655

Val Gly Gly Pro Ser Thr Leu Thr Ser Ala Gly Gln Leu Leu Pro Glu
660 665 670

Gly Thr Thr Thr Glu Thr Glu Ile Arg Lys Arg Arg Ser Ser Ser Tyr
675 680 685

His Val Ser Met Asp Leu Leu Glu Asp Pro Thr Ser Arg Gln Arg Ala
690 695 700

Met Ser Ile Ala Ser Ile Leu Thr Asn Thr Met Glu Glu Leu Glu Glu
705 710 715 720

Ser Arg Gln Lys Cys Pro Pro Cys Trp Tyr Lys Phe Ala Asn Met Cys
725 730 735

Leu Ile Trp Asp Cys Cys Lys Pro Trp Leu Lys Val Lys His Leu Val
740 745 750

SequencesSSCPRe-file7August03.ST25.txt

Asn Leu Val Val Met Asp Pro Phe Val Asp Leu Ala Ile Thr Ile Cys
755 760 765

Ile Val Leu Asn Thr Leu Phe Met Ala Met Glu His Tyr Pro Met Thr
770 775 780

Glu Gln Phe Ser Ser Val Leu Ser Val Gly Asn Leu Val Phe Thr Gly
785 790 795 800

Ile Phe Thr Ala Glu Met Phe Leu Lys Ile Ile Ala Met Asp Pro Tyr
805 810 815

Tyr Tyr Phe Gln Glu Gly Trp Asn Ile Phe Asp Gly Phe Ile Val Ser
820 825 830

Leu Ser Leu Met Glu Leu Gly Leu Ala Asn Val Glu Gly Leu Ser Val
835 840 845

Leu Arg Ser Phe Arg Leu Leu Arg Val Phe Lys Leu Ala Lys Ser Trp
850 855 860

Pro Thr Leu Asn Met Leu Ile Lys Ile Ile Gly Asn Ser Val Gly Ala
865 870 875 880

Leu Gly Asn Leu Thr Leu Val Leu Ala Ile Ile Val Phe Ile Phe Ala
885 890 895

Val Val Gly Met Gln Leu Phe Gly Lys Ser Tyr Lys Glu Cys Val Cys
900 905 910

Lys Ile Ser Asn Asp Cys Glu Leu Pro Arg Trp His Met His Asp Phe
915 920 925

Phe His Ser Phe Leu Ile Val Phe Arg Val Leu Cys Gly Glu Trp Ile
930 935 940

Glu Thr Met Trp Asp Cys Met Glu Val Ala Gly Gln Thr Met Cys Leu
945 950 955 960

Thr Val Phe Met Met Val Met Val Ile Gly Asn Leu Val Val Leu Asn
965 970 975

SequencesSSCPRe-file7August03.ST25.txt

Leu Phe Leu Ala Leu Leu Ser Ser Phe Ser Ser Asp Asn Leu Ala
980 985 990

Ala Thr Asp Asp Asp Asn Glu Met Asn Asn Ile Gln Ile Ala Val Gly
995 1000 1005

Arg Met Gln Lys Gly Ile Asp Phe Val Lys Arg Lys Ile Arg Glu
1010 1015 1020

Phe Ile Gln Lys Ala Phe Val Arg Lys Gln Lys Ala Leu Asp Glu
1025 1030 1035

Ile Lys Pro Leu Glu Asp Leu Asn Asn Lys Lys Asp Ser Cys Ile
1040 1045 1050

Ser Asn His Thr Thr Ile Glu Ile Gly Lys Asp Leu Asn Tyr Leu
1055 1060 1065

Lys Asp Gly Asn Gly Thr Thr Ser Gly Ile Gly Ser Ser Val Glu
1070 1075 1080

Lys Tyr Val Val Asp Glu Ser Asp Tyr Met Ser Phe Ile Asn Asn
1085 1090 1095

Pro Ser Leu Thr Val Thr Val Pro Ile Ala Val Gly Glu Ser Asp
1100 1105 1110

Phe Glu Asn Leu Asn Thr Glu Glu Phe Ser Ser Glu Ser Asp Met
1115 1120 1125

Glu Glu Ser Lys Glu Lys Leu Asn Ala Thr Ser Ser Ser Glu Gly
1130 1135 1140

Ser Thr Val Asp Ile Gly Ala Pro Ala Glu Gly Glu Gln Pro Glu
1145 1150 1155

Val Glu Pro Glu Glu Ser Leu Glu Pro Glu Ala Cys Phe Thr Glu
1160 1165 1170

Asp Cys Val Arg Lys Phe Lys Cys Cys Gln Ile Ser Ilé Glu Glu
Page 175

1175 SequencesSSCPre-file7August03.ST25.txt

1180

1185

Gly Lys Gly Lys Leu Trp Trp Asn Leu Arg Lys Thr Cys Tyr Lys
1190 1195 1200

Ile Val Glu His Asn Trp Phe Glu Thr Phe Ile Val Phe Met Ile
1205 1210 1215

Leu Leu Ser Ser Gly Ala Leu Ala Phe Glu Asp Ile Tyr Ile Glu
1220 1225 1230

Gln Arg Lys Thr Ile Lys Thr Met Leu Glu Tyr Ala Asp Lys Val
1235 1240 1245

Phe Thr Tyr Ile Phe Ile Leu Glu Met Leu Leu Lys Trp Val Ala
1250 1255 1260

Tyr Gly Phe Gln Val Tyr Phe Thr Asn Ala Trp Cys Trp Leu Asp
1265 1270 1275

Phe Leu Ile Val Asp Val Ser Leu Val Ser Leu Thr Ala Asn Ala
1280 1285 1290

Leu Gly Tyr Ser Glu Leu Gly Ala Ile Lys Ser Leu Arg Thr Leu
1295 1300 1305

Arg Ala Leu Arg Pro Leu Arg Ala Leu Ser Arg Phe Glu Gly Met
1310 1315 1320

Arg Val Val Val Asn Ala Leu Leu Gly Ala Ile Pro Ser Ile Met
1325 1330 1335

Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu Ile Phe Ser Ile
1340 1345 1350

Met Gly Val Asn Leu Phe Ala Gly Lys Phe Tyr His Cys Ile Asn
1355 1360 1365

Tyr Thr Thr Gly Glu Met Phe Asp Val Ser Val Val Asn Asn Tyr
1370 1375 1380

SequencesSSCPre-file7August03.ST25.txt

Ser Glu Cys Lys Ala Leu Ile Glu Ser Asn Gln Thr Ala Arg Trp
1385 1390 1395

Lys Asn Val Lys Val Asn Phe Asp Asn Val Gly Leu Gly Tyr Leu
1400 1405 1410

Ser Leu Leu Gln Val Ala Thr Phe Lys Gly Trp Met Asp Ile Met
1415 1420 1425

Tyr Ala Ala Val Asp Ser Arg Asn Val Glu Leu Gln Pro Lys Tyr
1430 1435 1440

Glu Asp Asn Leu Tyr Met Tyr Leu Tyr Phe Val Ile Phe Ile Ile
1445 1450 1455

Phe Gly Ser Phe Phe Thr Leu Asn Leu Phe Ile Gly Val Ile Ile
1460 1465 1470

Asp Asn Phe Asn Gln Gln Lys Lys Lys Phe Gly Gly Gln Asp Ile
1475 1480 1485

Phe Met Thr Glu Glu Gln Lys Lys Tyr Tyr Asn Ala Met Lys Lys
1490 1495 1500

Leu Gly Ser Lys Lys Pro Gln Lys Pro Ile Pro Arg Pro Ala Asn
1505 1510 1515

Lys Phe Gln Gly Met Val Phe Asp Phe Val Thr Lys Gln Val Phe
1520 1525 1530

Asp Ile Ser Ile Met Ile Leu Ile Cys Leu Asn Met Val Thr Met
1535 1540 1545

Met Val Glu Thr Asp Asp Gln Ser Gln Glu Met Thr Asn Ile Leu
1550 1555 1560

Tyr Trp Ile Asn Leu Val Phe Ile Val Leu Phe Thr Gly Glu Cys
1565 1570 1575

Val Leu Lys Leu Ile Ser Leu Arg Tyr Tyr Tyr Phe Thr Ile Gly
1580 1585 1590

SequencesSSCPre-file7August03.ST25.txt

Trp Asn Ile Phe Asp Phe Val Val Val Ile Leu Ser Ile Val Gly
1595 1600 1605

Met Phe Leu Ala Glu Leu Ile Glu Lys Tyr Phe Val Ser Pro Thr
1610 1615 1620

Leu Phe Arg Val Ile Arg Leu Ala Arg Ile Gly Arg Ile Leu Arg
1625 1630 1635

Leu Ile Lys Gly Ala Lys Gly Ile Arg Thr Leu Leu Phe Ala Leu
1640 1645 1650

Met Met Ser Leu Pro Ala Leu Phe Asn Ile Gly Leu Leu Leu Phe
1655 1660 1665

Leu Val Met Phe Ile Tyr Ala Ile Phe Gly Met Ser Asn Phe Ala
1670 1675 1680

Tyr Val Lys Arg Glu Val Gly Ile Asp Asp Met Phe Asn Phe Glu
1685 1690 1695

Thr Phe Gly Asn Ser Met Ile Cys Leu Phe Gln Ile Thr Thr Ser
1700 1705 1710

Ala Gly Trp Asp Gly Leu Leu Ala Pro Ile Leu Asn Ser Gly Pro
1715 1720 1725

Pro Asp Cys Asp Pro Asp Lys Asp His Pro Gly Ser Ser Val Lys
1730 1735 1740

Gly Asp Cys Gly Asn Pro Ser Val Gly Ile Phe Phe Phe Val Ser
1745 1750 1755

Tyr Ile Ile Ile Ser Phe Leu Val Val Leu Asn Met Tyr Ile Ala
1760 1765 1770

Val Ile Leu Glu Asn Phe Ser Val Ala Thr Glu Glu Ser Ala Glu
1775 1780 1785

Pro Leu Ser Glu Asp Asp Phe Glu Met Phe Tyr Glu Val Trp Glu
1790 1795 1800

SequencesSSCPre-file7August03.ST25.txt

Lys Phe Asp Pro Asp Ala Thr Gln Phe Ile Glu Phe Ala Lys Leu
1805 1810 1815

Ser Asp Phe Ala Asp Ala Leu Asp Pro Pro Leu Leu Ile Ala Lys
1820 1825 1830

Pro Asn Lys Val Gln Leu Ile Ala Met Asp Leu Pro Met Val Ser
1835 1840 1845

Gly Asp Arg Ile His Cys Leu Asp Ile Leu Phe Ala Phe Thr Lys
1850 1855 1860

Arg Val Leu Gly Glu Ser Gly Glu Met Asp Ala Leu Arg Ile Gln
1865 1870 1875

Met Glu Glu Arg Phe Met Ala Ser Asn Pro Ser Lys Val Ser Tyr
1880 1885 1890

Glu Pro Ile Thr Thr Leu Lys Arg Lys Gln Glu Glu Val Ser
1895 1900 1905

Ala Ile Ile Ile Gln Arg Ala Tyr Arg Arg Tyr Leu Leu Lys Gln
1910 1915 1920

Lys Val Lys Lys Val Ser Ser Ile Tyr Lys Lys Asp Lys Gly Lys
1925 1930 1935

Glu Cys Asp Gly Thr Pro Ile Lys Glu Asp Thr Leu Ile Asp Lys
1940 1945 1950

Leu Asn Glu Asn Ser Thr Pro Glu Lys Thr Asp Met Thr Pro Ser
1955 1960 1965

Thr Thr Ser Pro Pro Ser Tyr Asp Ser Val Thr Lys Pro Glu Lys
1970 1975 1980

Glu Lys Phe Glu Lys Asp Lys Ser Glu Lys Glu Asp Lys Gly Lys
1985 1990 1995

Asp Ile Arg Glu Ser Lys Lys

2000

SequencesSSCPRe-file7August03.ST25.txt
2005

<210> 67
<211> 2005
<212> PRT
<213> Homo sapiens

<400> 67

Met Ala Gln Ser Val Leu Val Pro Pro Gly Pro Asp Ser Phe Arg Phe
1 5 10 15

Phe Thr Arg Glu Ser Leu Ala Ala Ile Glu Gln Arg Ile Ala Glu Glu
20 25 30

Lys Ala Lys Arg Pro Lys Gln Glu Arg Lys Asp Glu Asp Asp Glu Asn
35 40 45

Gly Pro Lys Pro Asn Ser Asp Leu Glu Ala Gly Lys Ser Leu Pro Phe
50 55 60

Ile Tyr Gly Asp Ile Pro Pro Glu Met Val Ser Val Pro Leu Glu Asp
65 70 75 80

Leu Asp Pro Tyr Tyr Ile Asn Lys Lys Thr Phe Ile Val Leu Asn Lys
85 90 95

Gly Lys Ala Ile Ser Arg Phe Ser Ala Thr Pro Ala Leu Tyr Ile Leu
100 105 110

Thr Pro Phe Asn Pro Ile Arg Lys Leu Ala Ile Lys Ile Leu Val His
115 120 125

Ser Leu Phe Asn Met Leu Ile Met Cys Thr Ile Leu Thr Asn Cys Val
130 135 140

Phe Met Thr Met Ser Asn Pro Pro Asp Trp Thr Lys Asn Val Glu Tyr
145 150 155 160

Thr Phe Thr Gly Ile Tyr Thr Phe Glu Ser Leu Ile Lys Ile Leu Ala
165 170 175

Arg Gly Phe Cys Leu Glu Asp Phe Thr Phe Leu Arg Asp Pro Trp Asn

SequencesSSCPre-file7August03.ST25.txt
180 185 190

Trp Leu Asp Phe Thr Val Ile Thr Phe Ala Tyr Val Thr Glu Phe Val
195 200 205

Asp Leu Gly Asn Val Ser Ala Leu Arg Thr Phe Arg Val Leu Arg Ala
210 215 220

Leu Lys Thr Ile Ser Val Ile Pro Gly Leu Lys Thr Ile Val Gly Ala
225 230 235 240

Leu Ile Gln Ser Val Lys Lys Leu Ser Asp Val Met Ile Leu Thr Val
245 250 255

Phe Cys Leu Ser Val Phe Ala Leu Ile Gly Leu Gln Leu Phe Met Gly
260 265 270

Asn Leu Arg Asn Lys Cys Leu Gln Trp Pro Pro Asp Asn Ser Ser Phe
275 280 285

Glu Ile Asn Ile Thr Ser Phe Phe Asn Asn Ser Leu Asp Gly Asn Gly
290 295 300

Thr Thr Phe Asn Arg Thr Val Ser Ile Phe Asn Trp Asp Glu Tyr Ile
305 310 315 320

Glu Asp Lys Ser His Phe Tyr Phe Leu Glu Gly Gln Asn Asp Ala Leu
325 330 335

Leu Cys Gly Asn Ser Ser Asp Ala Gly Gln Cys Pro Glu Gly Tyr Ile
340 345 350

Cys Val Lys Ala Gly Arg Asn Pro Asn Tyr Gly Tyr Thr Ser Phe Asp
355 360 365

Thr Phe Ser Trp Ala Phe Leu Ser Leu Phe Arg Leu Met Thr Gln Asp
370 375 380

Phe Trp Glu Asn Leu Tyr Gln Leu Thr Leu Arg Ala Ala Gly Lys Thr
385 390 395 400

SequencesSSCPRe-file7August03.ST25.txt

Tyr Met Ile Phe Phe Val Leu Val Ile Phe Leu Gly Ser Phe Tyr Leu
405 410 415

Ile Asn Leu Ile Leu Ala Val Val Ala Met Ala Tyr Glu Glu Gln Asn
420 425 430

Gln Ala Thr Leu Glu Glu Ala Glu Gln Lys Glu Ala Glu Phe Gln Gln
435 440 445

Met Leu Glu Gln Leu Lys Lys Gln Gln Glu Glu Ala Gln Ala Ala Ala
450 455 460

Ala Ala Ala Ser Ala Glu Ser Arg Asp Phe Ser Gly Ala Gly Gly Ile
465 470 475 480

Gly Val Phe Ser Glu Ser Ser Ser Val Ala Ser Lys Leu Ser Ser Lys
485 490 495

Ser Glu Lys Glu Leu Lys Asn Arg Arg Lys Lys Lys Lys Gln Lys Glu
500 505 510

Gln Ser Gly Glu Glu Glu Lys Asn Asp Arg Val Leu Lys Ser Glu Ser
515 520 525

Glu Asp Ser Ile Arg Arg Lys Gly Phe Arg Phe Ser Leu Glu Gly Ser
530 535 540

Arg Leu Thr Tyr Glu Lys Arg Phe Ser Ser Pro His Gln Ser Leu Leu
545 550 555 560

Ser Ile Arg Gly Ser Leu Phe Ser Pro Arg Arg Asn Ser Arg Ala Ser
565 570 575

Leu Phe Ser Phe Arg Gly Arg Ala Lys Asp Ile Gly Ser Glu Asn Asp
580 585 590

Phe Ala Asp Asp Glu His Ser Thr Phe Glu Asp Asn Asp Ser Arg Arg
595 600 605

Asp Ser Leu Phe Val Pro His Arg His Gly Glu Arg Arg His Ser Asn
610 615 620

SequencesSSCPRe-file7August03.ST25.txt

Val Ser Gln Ala Ser Arg Ala Ser Arg Val Leu Pro Ile Leu Pro Met
625 630 635 640

Asn Gly Lys Met His Ser Ala Val Asp Cys Asn Gly Val Val Ser Leu
645 650 655

Val Gly Gly Pro Ser Thr Leu Thr Ser Ala Gly Gln Leu Leu Pro Glu
660 665 670

Gly Thr Thr Thr Glu Thr Glu Ile Arg Lys Arg Arg Ser Ser Ser Tyr
675 680 685

His Val Ser Met Asp Leu Leu Glu Asp Pro Thr Ser Arg Gln Arg Ala
690 695 700

Met Ser Ile Ala Ser Ile Leu Thr Asn Thr Met Glu Glu Leu Glu Glu
705 710 715 720

Ser Arg Gln Lys Cys Pro Pro Cys Trp Tyr Lys Phe Ala Asn Met Cys
725 730 735

Leu Ile Trp Asp Cys Cys Lys Pro Trp Leu Lys Val Lys His Leu Val
740 745 750

Asn Leu Val Val Met Asp Pro Phe Val Asp Leu Ala Ile Thr Ile Cys
755 760 765

Ile Val Leu Asn Thr Leu Phe Met Ala Met Glu His Tyr Pro Met Thr
770 775 780

Glu Gln Phe Ser Ser Val Leu Ser Val Gly Asn Leu Val Phe Thr Gly
785 790 795 800

Ile Phe Thr Ala Glu Met Phe Leu Lys Ile Ile Ala Met Asp Pro Tyr
805 810 815

Tyr Tyr Phe Gln Glu Gly Trp Asn Ile Phe Asp Gly Phe Ile Val Ser
820 825 830

Leu Ser Leu Met Glu Leu Gly Leu Ala Asn Val Glu Gly Leu Ser Val
835 840 845

SequencesSSCPRe-file7August03.ST25.txt

Leu Arg Ser Phe Arg Leu Leu Arg Val Phe Lys Leu Ala Lys Ser Trp
850 855 860

Pro Thr Leu Asn Met Leu Ile Lys Ile Ile Gly Asn Ser Val Gly Ala
865 870 875 880

Leu Gly Asn Leu Thr Leu Val Leu Ala Ile Ile Val Phe Ile Phe Ala
885 890 895

Val Val Gly Met Gln Leu Phe Gly Lys Ser Tyr Lys Glu Cys Val Cys
900 905 910

Lys Ile Ser Asn Asp Cys Glu Leu Pro Arg Trp His Met His Asp Phe
915 920 925

Phe His Ser Phe Leu Ile Val Phe Arg Val Leu Cys Gly Glu Trp Ile
930 935 940

Glu Thr Met Trp Asp Cys Met Glu Val Ala Gly Gln Thr Met Cys Leu
945 950 955 960

Thr Val Phe Met Met Val Met Val Ile Gly Asn Leu Val Val Leu Asn
965 970 975

Leu Phe Leu Ala Leu Leu Ser Ser Phe Ser Ser Asp Asn Leu Ala
980 985 990

Ala Thr Asp Asp Asp Asn Glu Met Asn Asn Leu Gln Ile Ala Val Gly
995 1000 1005

Arg Met Gln Lys Gly Ile Asp Phe Val Lys Arg Lys Ile Arg Glu
1010 1015 1020

Phe Ile Gln Lys Ala Phe Val Arg Lys Gln Lys Ala Leu Asp Glu
1025 1030 1035

Ile Lys Pro Leu Glu Asp Leu Asn Asn Lys Lys Asp Ser Cys Ile
1040 1045 1050

Ser Asn His Thr Thr Ile Glu Ile Gly Lys Asp Leu Asn Tyr Leu
Page 184

SequencesSSCPRe-file7August03.ST25.txt
1055 1060 1065

Lys Asp Gly Asn Gly Thr Thr Ser Gly Ile Gly Ser Ser Val Glu
1070 1075 1080

Lys Tyr Val Val Asp Glu Ser Asp Tyr Met Ser Phe Ile Asn Asn
1085 1090 1095

Pro Ser Leu Thr Val Thr Val Pro Ile Ala Val Gly Glu Ser Asp
1100 1105 1110

Phe Glu Asn Leu Asn Thr Glu Glu Phe Ser Ser Glu Ser Asp Met
1115 1120 1125

Glu Glu Ser Lys Glu Lys Leu Asn Ala Thr Ser Ser Ser Glu Gly
1130 1135 1140

Ser Thr Val Asp Ile Gly Ala Pro Ala Glu Gly Glu Gln Pro Glu
1145 1150 1155

Val Glu Pro Glu Glu Ser Leu Glu Pro Glu Ala Cys Phe Thr Glu
1160 1165 1170

Asp Cys Val Arg Lys Phe Lys Cys Cys Gln Ile Ser Ile Glu Glu
1175 1180 1185

Gly Lys Gly Lys Leu Trp Trp Asn Leu Arg Lys Ala Cys Tyr Lys
1190 1195 1200

Ile Val Glu His Asn Trp Phe Glu Thr Phe Ile Val Phe Met Ile
1205 1210 1215

Leu Leu Ser Ser Gly Ala Leu Ala Phe Glu Asp Ile Tyr Ile Glu
1220 1225 1230

Gln Arg Lys Thr Ile Lys Thr Met Leu Glu Tyr Ala Asp Lys Val
1235 1240 1245

Phe Thr Tyr Ile Phe Ile Leu Glu Met Leu Leu Lys Trp Val Ala
1250 1255 1260

SequencesSSCPRe-file7August03.ST25.txt

Tyr Gly Phe Gln Val Tyr Phe Thr Asn Ala Trp Cys Trp Leu Asp
1265 1270 1275

Phe Leu Ile Val Asp Val Ser Leu Val Ser Leu Thr Ala Asn Ala
1280 1285 1290

Leu Gly Tyr Ser Glu Leu Gly Ala Ile Lys Ser Leu Arg Thr Leu
1295 1300 1305

Arg Ala Leu Arg Pro Leu Arg Ala Leu Ser Arg Phe Glu Gly Met
1310 1315 1320

Arg Val Val Val Asn Ala Leu Leu Gly Ala Ile Pro Ser Ile Met
1325 1330 1335

Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu Ile Phe Ser Ile
1340 1345 1350

Met Gly Val Asn Leu Phe Ala Gly Lys Phe Tyr His Cys Ile Asn
1355 1360 1365

Tyr Thr Thr Gly Glu Met Phe Asp Val Ser Val Val Asn Asn Tyr
1370 1375 1380

Ser Glu Cys Lys Ala Leu Ile Glu Ser Asn Gln Thr Ala Arg Trp
1385 1390 1395

Lys Asn Val Lys Val Asn Phe Asp Asn Val Gly Leu Gly Tyr Leu
1400 1405 1410

Ser Leu Leu Gln Val Ala Thr Phe Lys Gly Trp Met Asp Ile Met
1415 1420 1425

Tyr Ala Ala Val Asp Ser Arg Asn Val Glu Leu Gln Pro Lys Tyr
1430 1435 1440

Glu Asp Asn Leu Tyr Met Tyr Leu Tyr Phe Val Ile Phe Ile Ile
1445 1450 1455

Phe Gly Ser Phe Phe Thr Leu Asn Leu Phe Ile Gly Val Ile Ile
1460 1465 1470

SequencesSSCPRe-file7August03.ST25.txt

Asp Asn Phe Asn Gln Gln Lys Lys Lys Phe Gly Gly Gln Asp Ile
1475 1480 1485

Phe Met Thr Glu Glu Gln Lys Lys Tyr Tyr Asn Ala Met Lys Lys
1490 1495 1500

Leu Gly Ser Lys Lys Pro Gln Lys Pro Ile Pro Arg Pro Ala Asn
1505 1510 1515

Lys Phe Gln Gly Met Val Phe Asp Phe Val Thr Lys Gln Val Phe
1520 1525 1530

Asp Ile Ser Ile Met Ile Leu Ile Cys Leu Asn Met Val Thr Met
1535 1540 1545

Met Val Glu Thr Asp Asp Gln Ser Gln Glu Met Thr Asn Ile Leu
1550 1555 1560

Tyr Trp Ile Asn Leu Val Phe Ile Val Leu Phe Thr Gly Glu Cys
1565 1570 1575

Val Leu Lys Leu Ile Ser Leu Arg Tyr Tyr Tyr Phe Thr Ile Gly
1580 1585 1590

Trp Asn Ile Phe Asp Phe Val Val Val Ile Leu Ser Ile Val Gly
1595 1600 1605

Met Phe Leu Ala Glu Leu Ile Glu Lys Tyr Phe Val Ser Pro Thr
1610 1615 1620

Leu Phe Arg Val Ile Arg Leu Ala Arg Ile Gly Arg Ile Leu Arg
1625 1630 1635

Leu Ile Lys Gly Ala Lys Gly Ile Arg Thr Leu Leu Phe Ala Leu
1640 1645 1650

Met Met Ser Leu Pro Ala Leu Phe Asn Ile Gly Leu Leu Leu Phe
1655 1660 1665

Leu Val Met Phe Ile Tyr Ala Ile Phe Gly Met Ser Asn Phe Ala
1670 1675 1680

SequencesSSCPRe-file7August03.ST25.txt

Tyr Val Lys Arg Glu Val Gly Ile Asp Asp Met Phe Asn Phe Glu
1685 1690 1695

Thr Phe Gly Asn Ser Met Ile Cys Leu Phe Gln Ile Thr Thr Ser
1700 1705 1710

Ala Gly Trp Asp Gly Leu Leu Ala Pro Ile Leu Asn Ser Gly Pro
1715 1720 1725

Pro Asp Cys Asp Pro Asp Lys Asp His Pro Gly Ser Ser Val Lys
1730 1735 1740

Gly Asp Cys Gly Asn Pro Ser Val Gly Ile Phe Phe Phe Val Ser
1745 1750 1755

Tyr Ile Ile Ile Ser Phe Leu Val Val Leu Asn Met Tyr Ile Ala
1760 1765 1770

Val Ile Leu Glu Asn Phe Ser Val Ala Thr Glu Glu Ser Ala Glu
1775 1780 1785

Pro Leu Ser Glu Asp Asp Phe Glu Met Phe Tyr Glu Val Trp Glu
1790 1795 1800

Lys Phe Asp Pro Asp Ala Thr Gln Phe Ile Glu Phe Ala Lys Leu
1805 1810 1815

Ser Asp Phe Ala Asp Ala Leu Asp Pro Pro Leu Leu Ile Ala Lys
1820 1825 1830

Pro Asn Lys Val Gln Leu Ile Ala Met Asp Leu Pro Met Val Ser
1835 1840 1845

Gly Asp Arg Ile His Cys Leu Asp Ile Leu Phe Ala Phe Thr Lys
1850 1855 1860

Arg Val Leu Gly Glu Ser Gly Glu Met Asp Ala Leu Arg Ile Gln
1865 1870 1875

Met Glu Glu Arg Phe Met Ala Ser Asn Pro Ser Lys Val Ser Tyr

1880

SequencesSSCPre-file7August03.ST25.txt
1885
1890

Glu Pro Ile Thr Thr Thr Leu Lys Arg Lys Gln Glu Glu Val Ser
1895 1900 1905

Ala Ile Ile Ile Gln Arg Ala Tyr Arg Arg Tyr Leu Leu Lys Gln
1910 1915 1920

Lys Val Lys Lys Val Ser Ser Ile Tyr Lys Lys Asp Lys Gly Lys
1925 1930 1935

Glu Cys Asp Gly Thr Pro Ile Lys Glu Asp Thr Leu Ile Asp Lys
1940 1945 1950

Leu Asn Glu Asn Ser Thr Pro Glu Lys Thr Asp Met Thr Pro Ser
1955 1960 1965

Thr Thr Ser Pro Pro Ser Tyr Asp Ser Val Thr Lys Pro Glu Lys
1970 1975 1980

Glu Lys Phe Glu Lys Asp Lys Ser Glu Lys Glu Asp Lys Gly Lys
1985 1990 1995

Asp Ile Arg Glu Ser Lys Lys
2000 2005

<210> 68

<211> 2005

<212> PRT

<213> Homo sapiens

<400> 68

Met Ala Gln Ser Val Leu Val Pro Pro Gly Pro Asp Ser Phe Arg Phe
1 5 10 15

Phe Thr Arg Glu Ser Leu Ala Ala Ile Glu Gln Arg Ile Ala Glu Glu
20 25 30

Lys Ala Lys Arg Pro Lys Gln Glu Arg Lys Asp Glu Asp Asp Glu Asn
35 40 45

Gly Pro Lys Pro Asn Ser Asp Leu Glu Ala Gly Lys Ser Leu Pro Phe

SequencesSSCPPre-file7August03.ST25.txt
55 60

Ile Tyr Gly Asp Ile Pro Pro Glu Met Val Ser Val Pro Leu Glu Asp
65 70 75 80

Gly Lys Ala Ile Ser Arg Phe Ser Ala Thr Pro Ala Leu Tyr Ile Leu
100 105 110

Thr Pro Phe Asn Pro Ile Arg Lys Leu Ala Ile Lys Ile Leu Val His
115 120 125

Ser Leu Phe Asn Met Leu Ile Met Cys Thr Ile Leu Thr Asn Cys Val
130 135 140

Phe Met Thr Met Ser Asn Pro Pro Asp Trp Thr Lys Asn Val Glu Tyr
 145 150 155 160

Thr Phe Thr Gly Ile Tyr Thr Phe Glu Ser Leu Ile Lys Ile Leu Ala
165 170 . 175

Arg Gly Phe Cys Leu Glu Asp Phe Thr Phe Leu Arg Asp Pro Trp Asn
180 185 190

Trp Leu Asp Phe Thr Val Ile Thr Phe Ala Tyr Val Thr Glu Phe Val
195 200 205

Asp Leu Gly Asn Val Ser Ala Leu Arg Thr Phe Arg Val Leu Arg Ala
210 215 220

Leu Lys Thr Ile Ser Val Ile Pro Gly Leu Lys Thr Ile Val Gly Ala
225 230 235 240

Leu Ile Gln Ser Val Lys Lys Leu Ser Asp Val Met Ile Leu Thr Val
245 250 255

Phe Cys Leu Ser Val Phe Ala Leu Ile Gly Leu Gln Leu Phe Met Gly
 260 265 . 270

SequencesSSCPre-file7August03.ST25.txt

Asn Leu Arg Asn Lys Cys Leu Gln Trp Pro Pro Asp Asn Ser Ser Phe
275 280 285

Glu Ile Asn Ile Thr Ser Phe Phe Asn Asn Ser Leu Asp Gly Asn Gly
290 295 300

Thr Thr Phe Asn Arg Thr Val Ser Ile Phe Asn Trp Asp Glu Tyr Ile
305 310 315 320

Glu Asp Lys Ser His Phe Tyr Phe Leu Glu Gly Gln Asn Asp Ala Leu
325 330 335

Leu Cys Gly Asn Ser Ser Asp Ala Gly Gln Cys Pro Glu Gly Tyr Ile
340 345 350

Cys Val Lys Ala Gly Arg Asn Pro Asn Tyr Gly Tyr Thr Ser Phe Asp
355 360 365

Thr Phe Ser Trp Ala Phe Leu Ser Leu Phe Arg Leu Met Thr Gln Asp
370 375 380

Phe Trp Glu Asn Leu Tyr Gln Leu Thr Leu Arg Ala Ala Gly Lys Thr
385 390 395 400

Tyr Met Ile Phe Phe Val Leu Val Ile Phe Leu Gly Ser Phe Tyr Leu
405 410 415

Ile Asn Leu Ile Leu Ala Val Val Ala Met Ala Tyr Glu Glu Gln Asn
420 425 430

Gln Ala Thr Leu Glu Glu Ala Glu Gln Lys Glu Ala Glu Phe Gln Gln
435 440 445

Met Leu Glu Gln Leu Lys Gln Gln Glu Ala Gln Ala Ala Ala
450 455 460

Ala Ala Ala Ser Ala Glu Ser Arg Asp Phe Ser Gly Ala Gly Gly Ile
465 470 475 480

Gly Val Phe Ser Glu Ser Ser Ser Val Ala Ser Lys Leu Ser Ser Lys
485 490 495

SequencesSSCPRe-file7August03.ST25.txt

Ser Glu Lys Glu Leu Lys Asn Arg Arg Lys Lys Lys Lys Gln Lys Glu
500 505 510

Gln Ser Gly Glu Glu Glu Lys Asn Asp Arg Val Leu Lys Ser Glu Ser
515 520 525

Glu Asp Ser Ile Arg Arg Lys Gly Phe Arg Phe Ser Leu Glu Gly Ser
530 535 540

Arg Leu Thr Tyr Glu Lys Arg Phe Ser Ser Pro His Gln Ser Leu Leu
545 550 555 560

Ser Ile Arg Gly Ser Leu Phe Ser Pro Arg Arg Asn Ser Arg Ala Ser
565 570 575

Leu Phe Ser Phe Arg Gly Arg Ala Lys Asp Ile Gly Ser Glu Asn Asp
580 585 590

Phe Ala Asp Asp Glu His Ser Thr Phe Glu Asp Asn Asp Ser Arg Arg
595 600 605

Asp Ser Leu Phe Val Pro His Arg His Gly Glu Arg Arg His Ser Asn
610 615 620

Val Ser Gln Ala Ser Arg Ala Ser Arg Val Leu Pro Ile Leu Pro Met
625 630 635 640

Asn Gly Lys Met His Ser Ala Val Asp Cys Asn Gly Val Val Ser Leu
645 650 655

Val Gly Gly Pro Ser Thr Leu Thr Ser Ala Gly Gln Leu Leu Pro Glu
660 665 670

Gly Thr Thr Thr Glu Thr Glu Ile Arg Lys Arg Arg Ser Ser Ser Tyr
675 680 685

His Val Ser Met Asp Leu Leu Glu Asp Pro Thr Ser Arg Gln Arg Ala
690 695 700

Met Ser Ile Ala Ser Ile Leu Thr Asn Thr Met Glu Glu Leu Glu Glu
705 710 715 720

SequencesSSCPre-file7August03.ST25.txt

Ser Arg Gln Lys Cys Pro Pro Cys Trp Tyr Lys Phe Ala Asn Met Cys
725 730 735

Leu Ile Trp Asp Cys Cys Lys Pro Trp Leu Lys Val Lys His Leu Val
740 745 750

Asn Leu Val Val Met Asp Pro Phe Val Asp Leu Ala Ile Thr Ile Cys
755 760 765

Ile Val Leu Asn Thr Leu Phe Met Ala Met Glu His Tyr Pro Met Thr
770 775 780

Glu Gln Phe Ser Ser Val Leu Ser Val Gly Asn Leu Val Phe Thr Gly
785 790 795 800

Ile Phe Thr Ala Glu Met Phe Leu Lys Ile Ile Ala Met Asp Pro Tyr
805 810 815

Tyr Tyr Phe Gln Glu Gly Trp Asn Ile Phe Asp Gly Phe Ile Val Ser
820 825 830

Leu Ser Leu Met Glu Leu Gly Leu Ala Asn Val Glu Gly Leu Ser Val
835 840 845

Leu Arg Ser Phe Arg Leu Leu Arg Val Phe Lys Leu Ala Lys Ser Trp
850 855 860

Pro Thr Leu Asn Met Leu Ile Lys Ile Ile Gly Asn Ser Val Gly Ala
865 870 875 880

Leu Gly Asn Leu Thr Leu Val Leu Ala Ile Ile Val Phe Ile Phe Ala
885 890 895

Val Val Gly Met Gln Leu Phe Gly Lys Ser Tyr Lys Glu Cys Val Cys
900 905 910

Lys Ile Ser Asn Asp Cys Glu Leu Pro Arg Trp His Met His Asp Phe
915 920 925

Phe His Ser Phe Leu Ile Val Phe Arg Val Leu Cys Gly Glu Trp Ile

930

SequencesSSCPre-file7August03.ST25.txt
935 940

Glu Thr Met Trp Asp Cys Met Glu Val Ala Gly Gln Thr Met Cys Leu
945 950 955 960

Thr Val Phe Met Met Val Met Val Ile Gly Asn Leu Val Val Leu Asn
965 970 975

Leu Phe Leu Ala Leu Leu Ser Ser Phe Ser Ser Asp Asn Leu Ala
980 985 990

Ala Thr Asp Asp Asp Asn Glu Met Asn Asn Leu Gln Ile Ala Val Gly
995 1000 1005

Arg Met Gln Lys Gly Ile Asp Phe Val Lys Arg Lys Ile Arg Glu
1010 1015 1020

Phe Ile Gln Lys Ala Phe Val Arg Lys Gln Lys Ala Leu Asp Glu
1025 1030 1035

Ile Lys Pro Leu Glu Asp Leu Asn Asn Lys Lys Asp Ser Cys Ile
1040 1045 1050

Ser Asn His Thr Thr Ile Glu Ile Gly Lys Asp Leu Asn Tyr Leu
1055 1060 1065

Lys Asp Gly Asn Gly Thr Thr Ser Gly Ile Gly Ser Ser Val Glu
1070 1075 1080

Lys Tyr Val Val Asp Glu Ser Asp Tyr Met Ser Phe Ile Asn Asn
1085 1090 1095

Pro Ser Leu Thr Val Thr Val Pro Ile Ala Val Gly Glu Ser Asp
1100 1105 1110

Phe Glu Asn Leu Asn Thr Glu Glu Phe Ser Ser Glu Ser Asp Met
1115 1120 1125

Glu Glu Ser Lys Glu Lys Leu Asn Ala Thr Ser Ser Ser Glu Gly
1130 1135 1140

SequencesSSCPre-file7August03.ST25.txt

Ser Thr Val Asp Ile Gly Ala Pro Ala Glu Gly Glu Gln Pro Glu
1145 1150 1155

Val Glu Pro Glu Glu Ser Leu Glu Pro Glu Ala Cys Phe Thr Glu
1160 1165 1170

Asp Cys Val Arg Lys Phe Lys Cys Cys Gln Ile Ser Ile Glu Glu
1175 1180 1185

Gly Lys Gly Lys Leu Trp Trp Asn Leu Arg Lys Thr Cys Tyr Lys
1190 1195 1200

Ile Val Glu His Asn Trp Phe Glu Thr Phe Ile Val Phe Met Ile
1205 1210 1215

Leu Leu Ser Ser Gly Ala Leu Ala Phe Glu Asp Ile Tyr Ile Glu
1220 1225 1230

Gln Arg Lys Thr Ile Lys Thr Met Leu Glu Tyr Ala Asp Lys Val
1235 1240 1245

Phe Thr Tyr Ile Phe Ile Leu Glu Met Leu Leu Lys Trp Val Ala
1250 1255 1260

Tyr Gly Phe Gln Val Tyr Phe Thr Asn Ala Trp Cys Trp Leu Asp
1265 1270 1275

Phe Leu Ile Val Asp Val Ser Leu Val Ser Leu Thr Ala Asn Ala
1280 1285 1290

Leu Gly Tyr Ser Glu Leu Gly Ala Ile Lys Ser Leu Arg Thr Leu
1295 1300 1305

Arg Ala Leu Arg Pro Leu Arg Ala Leu Ser Gln Phe Glu Gly Met
1310 1315 1320

Arg Val Val Val Asn Ala Leu Leu Gly Ala Ile Pro Ser Ile Met
1325 1330 1335

Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu Ile Phe Ser Ile
1340 1345 1350

SequencesSSCPre-file7August03.ST25.txt

Met Gly Val Asn Leu Phe Ala Gly Lys Phe Tyr His Cys Ile Asn
1355 1360 1365

Tyr Thr Thr Gly Glu Met Phe Asp Val Ser Val Val Asn Asn Tyr
1370 1375 1380

Ser Glu Cys Lys Ala Leu Ile Glu Ser Asn Gln Thr Ala Arg Trp
1385 1390 1395

Lys Asn Val Lys Val Asn Phe Asp Asn Val Gly Leu Gly Tyr Leu
1400 1405 1410

Ser Leu Leu Gln Val Ala Thr Phe Lys Gly Trp Met Asp Ile Met
1415 1420 1425

Tyr Ala Ala Val Asp Ser Arg Asn Val Glu Leu Gln Pro Lys Tyr
1430 1435 1440

Glu Asp Asn Leu Tyr Met Tyr Leu Tyr Phe Val Ile Phe Ile Ile
1445 1450 1455

Phe Gly Ser Phe Phe Thr Leu Asn Leu Phe Ile Gly Val Ile Ile
1460 1465 1470

Asp Asn Phe Asn Gln Gln Lys Lys Lys Phe Gly Gly Gln Asp Ile
1475 1480 1485

Phe Met Thr Glu Glu Gln Lys Lys Tyr Tyr Asn Ala Met Lys Lys
1490 1495 1500

Leu Gly Ser Lys Lys Pro Gln Lys Pro Ile Pro Arg Pro Ala Asn
1505 1510 1515

Lys Phe Gln Gly Met Val Phe Asp Phe Val Thr Lys Gln Val Phe
1520 1525 1530

Asp Ile Ser Ile Met Ile Leu Ile Cys Leu Asn Met Val Thr Met
1535 1540 1545

Met Val Glu Thr Asp Asp Gln Ser Gln Glu Met Thr Asn Ile Leu
1550 1555 1560

SequencesSSCPRe-file7August03.ST25.txt

Tyr Trp Ile Asn Leu Val Phe Ile Val Leu Phe Thr Gly Glu Cys
1565 1570 1575

Val Leu Lys Leu Ile Ser Leu Arg Tyr Tyr Tyr Phe Thr Ile Gly
1580 1585 1590

Trp Asn Ile Phe Asp Phe Val Val Val Ile Leu Ser Ile Val Gly
1595 1600 1605

Met Phe Leu Ala Glu Leu Ile Glu Lys Tyr Phe Val Ser Pro Thr
1610 1615 1620

Leu Phe Arg Val Ile Arg Leu Ala Arg Ile Gly Arg Ile Leu Arg
1625 1630 1635

Leu Ile Lys Gly Ala Lys Gly Ile Arg Thr Leu Leu Phe Ala Leu
1640 1645 1650

Met Met Ser Leu Pro Ala Leu Phe Asn Ile Gly Leu Leu Leu Phe
1655 1660 1665

Leu Val Met Phe Ile Tyr Ala Ile Phe Gly Met Ser Asn Phe Ala
1670 1675 1680

Tyr Val Lys Arg Glu Val Gly Ile Asp Asp Met Phe Asn Phe Glu
1685 1690 1695

Thr Phe Gly Asn Ser Met Ile Cys Leu Phe Gln Ile Thr Thr Ser
1700 1705 1710

Ala Gly Trp Asp Gly Leu Leu Ala Pro Ile Leu Asn Ser Gly Pro
1715 1720 1725

Pro Asp Cys Asp Pro Asp Lys Asp His Pro Gly Ser Ser Val Lys
1730 1735 1740

Gly Asp Cys Gly Asn Pro Ser Val Gly Ile Phe Phe Val Ser
1745 1750 1755

Tyr Ile Ile Ile Ser Phe Leu Val Val Leu Asn Met Tyr Ile Ala

SequencesSSCPre-file7August03.ST25.txt
1760 1765 1770

Val Ile Leu Glu Asn Phe Ser Val Ala Thr Glu Glu Ser Ala Glu
1775 1780 1785

Pro Leu Ser Glu Asp Asp Phe Glu Met Phe Tyr Glu Val Trp Glu
1790 1795 1800

Lys Phe Asp Pro Asp Ala Thr Gln Phe Ile Glu Phe Ala Lys Leu
1805 1810 1815

Ser Asp Phe Ala Asp Ala Leu Asp Pro Pro Leu Leu Ile Ala Lys
1820 1825 1830

Pro Asn Lys Val Gln Leu Ile Ala Met Asp Leu Pro Met Val Ser
1835 1840 1845

Gly Asp Arg Ile His Cys Leu Asp Ile Leu Phe Ala Phe Thr Lys
1850 1855 1860

Arg Val Leu Gly Glu Ser Gly Glu Met Asp Ala Leu Arg Ile Gln
1865 1870 1875

Met Glu Glu Arg Phe Met Ala Ser Asn Pro Ser Lys Val Ser Tyr
1880 1885 1890

Glu Pro Ile Thr Thr Leu Lys Arg Lys Gln Glu Glu Val Ser
1895 1900 1905

Ala Ile Ile Ile Gln Arg Ala Tyr Arg Arg Tyr Leu Leu Lys Gln
1910 1915 1920

Lys Val Lys Lys Val Ser Ser Ile Tyr Lys Lys Asp Lys Gly Lys
1925 1930 1935

Glu Cys Asp Gly Thr Pro Ile Lys Glu Asp Thr Leu Ile Asp Lys
1940 1945 1950

Leu Asn Glu Asn Ser Thr Pro Glu Lys Thr Asp Met Thr Pro Ser
1955 1960 1965

SequencesSSCPre-file7August03.ST25.txt

Thr Thr Ser Pro Pro Ser Tyr Asp Ser Val Thr Lys Pro Glu Lys
1970 1975 1980

Glu Lys Phe Glu Lys Asp Lys Ser Glu Lys Glu Asp Lys Gly Lys
1985 1990 1995

Asp Ile Arg Glu Ser Lys Lys
2000 2005

<210> 69
<211> 468
<212> PRT
<213> Homo sapiens

<400> 69

Met Ala Ala Arg Gly Ser Gly Pro Arg Ala Leu Arg Leu Leu Leu
1 5 10 15

Val Gln Leu Val Ala Gly Ala Leu Arg Ser Ser Arg Ala Arg Arg Ala
20 25 30

Ala Arg Arg Gly Leu Ser Glu Pro Ser Ser Ile Ala Lys His Glu Asp
35 40 45

Ser Leu Leu Lys Asp Leu Phe Gln Asp Tyr Glu Arg Trp Val Arg Pro
50 55 60

Val Glu His Leu Asn Asp Lys Ile Lys Ile Lys Phe Gly Leu Ala Ile
65 70 75 80

Ser Gln Leu Val Asp Val Asp Glu Lys Asn Gln Leu Met Thr Thr Asn
85 90 95

Val Trp Leu Lys Gln Glu Trp Ile Asp Val Lys Leu Arg Trp Asn Pro
100 105 110

Asp Asp Tyr Gly Gly Ile Lys Val Ile Arg Val Pro Ser Asp Ser Ser
115 120 125

Trp Thr Pro Asp Ile Ile Leu Phe Asp Asn Ala Asp Gly Arg Phe Glu
130 135 140

SequencesSSCPRe-file7August03.ST25.txt

Gly Thr Ser Thr Lys Thr Val Ile Arg Tyr Asn Gly Thr Val Thr Trp
145 150 155 160

Thr Pro Pro Ala Asn Tyr Lys Ser Ser Cys Thr Ile Asp Val Thr Phe
165 170 175

Phe Pro Phe Asp Leu Gln Asn Cys Ser Met Lys Phe Gly Ser Trp Thr
180 185 190

Tyr Asp Gly Ser Gln Val Asp Ile Ile Leu Glu Asp Gln Asp Val Asp
195 200 205

Lys Arg Asp Phe Phe Asp Asn Gly Glu Trp Glu Ile Val Ser Ala Thr
210 215 220

Gly Ser Lys Gly Asn Arg Thr Asp Ser Cys Cys Trp Tyr Pro Tyr Val
225 230 235 240

Thr Tyr Ser Phe Val Ile Lys Arg Leu Pro Leu Phe Tyr Thr Leu Phe
245 250 255

Leu Ile Ile Pro Cys Ile Gly Leu Ser Phe Leu Thr Val Leu Val Phe
260 265 270

Tyr Leu Pro Ser Asn Glu Gly Glu Lys Ile Cys Leu Cys Thr Ser Val
275 280 285

Leu Val Ser Leu Thr Val Phe Leu Leu Val Ile Glu Glu Ile Ile Pro
290 295 300

Ser Ser Ser Lys Val Ile Pro Leu Ile Gly Glu Tyr Leu Val Phe Thr
305 310 315 320

Met Ile Phe Val Thr Leu Ser Ile Met Val Thr Val Phe Ala Ile Asn
325 330 335

Ile His His Arg Ser Ser Thr His Asn Ala Met Ala Pro Leu Val
340 345 350

Arg Lys Ile Phe Leu His Thr Leu Pro Lys Leu Leu Ser Met Arg Ser
355 360 365

SequencesSSCPRe-file7August03.ST25.txt

His Val Asp Arg Tyr Phe Thr Gln Lys Glu Glu Thr Glu Ser Gly Ser
370 375 380

Gly Pro Lys Ser Ser Arg Asn Thr Leu Glu Ala Ala Leu Asp Ser Ile
385 390 395 400

Arg Tyr Ile Thr Thr His Ile Met Lys Glu Asn Asp Val Arg Glu Val
405 410 415

Val Glu Asp Trp Lys Phe Ile Ala Gln Val Leu Asp Arg Met Phe Leu
420 425 430

Trp Thr Phe Leu Phe Val Ser Ile Val Gly Ser Leu Gly Leu Phe Val
435 440 445

Pro Val Ile Tyr Lys Trp Ala Asn Ile Leu Ile Pro Val His Ile Gly
450 455 460

Asn Ala Asn Lys
465

<210> 70
<211> 529
<212> PRT
<213> Homo sapiens

<400> 70

Met Gly Pro Ser Cys Pro Val Phe Leu Ser Phe Thr Lys Leu Ser Leu
1 5 10 15

Trp Trp Leu Leu Leu Thr Pro Ala Gly Gly Glu Glu Ala Lys Arg Pro
20 25 30

Pro Pro Arg Ala Pro Gly Asp Pro Leu Ser Ser Pro Ser Pro Thr Ala
35 40 45

Leu Pro Gln Gly Gly Ser His Thr Glu Thr Glu Asp Arg Leu Phe Lys
50 55 60

His Leu Phe Arg Gly Tyr Asn Arg Trp Ala Arg Pro Val Pro Asn Thr
65 70 75 80

SequencesSSCPre-file7August03.ST25.txt

Ser Asp Val Val Ile Val Arg Phe Gly Leu Ser Ile Ala Gln Leu Ile
85 90 95

Asp Val Asp Glu Lys Asn Gln Met Met Thr Thr Asn Val Trp Leu Lys
100 105 110

Gln Glu Trp Ser Asp Tyr Lys Leu Arg Trp Asn Pro Thr Asp Phe Gly
115 120 125

Asn Ile Thr Ser Leu Arg Val Pro Ser Glu Met Ile Trp Ile Pro Asp
130 135 140

Ile Val Leu Tyr Asn Asn Ala Asp Gly Glu Phe Ala Val Thr His Met
145 150 155 160

Thr Lys Ala His Leu Phe Ser Thr Gly Thr Val His Trp Val Pro Pro
165 170 175

Ala Ile Tyr Lys Ser Ser Cys Ser Ile Asp Val Thr Phe Phe Pro Phe
180 185 190

Asp Gln Gln Asn Cys Lys Met Lys Phe Gly Ser Trp Thr Tyr Asp Lys
195 200 205

Ala Lys Ile Asp Leu Glu Gln Met Glu Gln Thr Val Asp Leu Lys Asp
210 215 220

Tyr Trp Glu Ser Gly Glu Trp Ala Ile Val Asn Ala Thr Gly Thr Tyr
225 230 235 240

Asn Ser Lys Lys Tyr Asp Cys Cys Ala Glu Ile Tyr Pro Asp Val Thr
245 250 255

Tyr Ala Phe Val Ile Arg Arg Leu Pro Leu Phe Tyr Thr Ile Asn Leu
260 265 270

Ile Ile Pro Cys Leu Leu Ile Ser Cys Leu Thr Val Leu Val Phe Tyr
275 280 285

Leu Pro Ser Asp Cys Gly Glu Lys Ile Thr Leu Cys Ile Ser Val Leu
290 295 300

SequencesSSCPRe-file7August03.ST25.txt

Leu Ser Leu Thr Val Phe Leu Leu Leu Ile Thr Glu Ile Ile Pro Ser
305 310 315 320

Thr Ser Leu Val Ile Pro Leu Ile Gly Glu Tyr Leu Leu Phe Thr Met
325 330 335

Ile Phe Val Thr Leu Ser Ile Val Ile Thr Val Phe Val Leu Asn Val
340 345 350

His His Arg Ser Pro Ser Thr His Thr Met Pro His Trp Val Arg Gly
355 360 365

Ala Leu Leu Gly Cys Val Pro Arg Trp Leu Leu Met Asn Arg Pro Pro
370 375 380

Pro Pro Val Glu Leu Cys His Pro Leu Arg Leu Lys Leu Ser Pro Ser
385 390 395 400

Tyr His Trp Leu Glu Ser Asn Val Asp Ala Glu Glu Arg Glu Val Val
405 410 415

Val Glu Glu Glu Asp Arg Trp Ala Cys Ala Gly His Val Ala Pro Ser
420 425 430

Val Gly Thr Leu Cys Ser His Gly His Leu His Ser Gly Ala Ser Gly
435 440 445

Pro Lys Ala Glu Ala Leu Leu Gln Glu Gly Glu Leu Leu Leu Ser Pro
450 455 460

His Met Gln Lys Ala Leu Glu Gly Val His Tyr Ile Ala Asp His Leu
465 470 475 480

Arg Ser Glu Asp Ala Asp Ser Ser Val Lys Glu Asp Trp Lys Tyr Val
485 490 495

Ala Met Val Ile Asp Arg Ile Phe Leu Trp Leu Phe Ile Ile Val Cys
500 505 510

Phe Leu Gly Thr Ile Gly Leu Phe Leu Pro Pro Phe Leu Ala Gly Met

515 SequencesSSCPre-file7August03.ST25.txt
520 525

Ile

<210> 71
<211> 505
<212> PRT
<213> Homo sapiens

<400> 71

Met Gly Ser Gly Pro Leu Ser Leu Pro Leu Ala Leu Ser Pro Pro Arg
1 5 10 15

Leu Leu Leu Leu Leu Leu Ser Leu Leu Pro Val Ala Arg Ala Ser
20 25 30

Glu Ala Glu His His Leu Phe Glu Arg Leu Phe Glu Asp Tyr Asn Glu
35 40 45

Ile Ile Arg Pro Val Ala Asn Val Ser Asp Pro Val Ile Ile His Phe
50 55 60

Glu Val Ser Met Ser Gln Leu Val Lys Val Asp Glu Val Asn Gln Ile
65 70 75 80

Met Glu Thr Asn Leu Trp Leu Lys Gln Ile Trp Asn Asp Tyr Lys Leu
85 90 95

Lys Trp Asn Pro Ser Asp Tyr Gly Gly Ala Glu Phe Met Arg Val Pro
100 105 110

Ala Gln Lys Ile Trp Lys Pro Asp Ile Val Leu Tyr Asn Asn Ala Val
115 120 125

Gly Asp Phe Gln Val Asp Asp Lys Thr Lys Ala Leu Leu Lys Tyr Thr
130 135 140

Gly Glu Val Thr Trp Ile Pro Pro Ala Ile Phe Lys Ser Ser Cys Lys
145 150 155 160

Ile Asp Val Thr Tyr Phe Pro Phe Asp Tyr Gln Asn Cys Thr Met Lys

SequencesSSCPre-file7August03.ST25.txt

165

170

175

Phe Gly Ser Trp Ser Tyr Asp Lys Ala Lys Ile Asp Leu Val Leu Ile
180 185 190

Gly Ser Ser Met Asn Leu Lys Asp Tyr Trp Glu Ser Gly Glu Trp Ala
195 200 205

Ile Ile Lys Ala Pro Gly Tyr Lys His Asp Ile Lys Tyr Asn Cys Cys
210 215 220

Glu Glu Ile Tyr Pro Asp Ile Thr Tyr Ser Leu Tyr Ile Arg Arg Leu
225 230 235 240

Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Leu Ile Ser
245 250 255

Phe Leu Thr Val Leu Val Phe Tyr Leu Pro Ser Asp Cys Gly Glu Lys
260 265 270

Val Thr Leu Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe Leu Leu
275 280 285

Val Ile Thr Glu Thr Ile Pro Ser Thr Ser Leu Val Ile Pro Leu Ile
290 295 300

Gly Glu Tyr Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Val
305 310 315 320

Ile Thr Val Phe Val Leu Asn Val His Tyr Arg Thr Pro Thr Thr His
325 330 335

Thr Met Pro Ser Trp Val Lys Thr Val Phe Leu Asn Leu Leu Pro Arg
340 345 350

Val Met Phe Met Thr Arg Pro Thr Ser Asn Glu Gly Asn Ala Gln Lys
355 360 365

Pro Arg Pro Leu Tyr Gly Ala Glu Leu Ser Asn Leu Asn Cys Phe Ser
370 375 380

SequencesSSCPre-file7August03.ST25.txt

Arg Ala Glu Ser Lys Gly Cys Lys Glu Gly Tyr Pro Cys Gln Asp Gly
385 390 395 400

Met Cys Gly Tyr Cys His His Arg Arg Ile Lys Ile Ser Asn Phe Ser
405 410 415

Ala Asn Leu Thr Arg Ser Ser Ser Glu Ser Val Asp Ala Val Leu
420 425 430

Ser Leu Ser Ala Leu Ser Pro Glu Ile Lys Glu Ala Ile Gln Ser Val
435 440 445

Lys Tyr Ile Ala Glu Asn Met Lys Ala Gln Asn Glu Ala Lys Glu Ile
450 455 460

Gln Asp Asp Trp Lys Tyr Val Ala Met Val Ile Asp Arg Ile Phe Leu
465 470 475 480

Trp Val Phe Thr Leu Val Cys Ile Leu Gly Thr Ala Gly Leu Phe Leu
485 490 495

Gln Pro Leu Met Ala Arg Glu Asp Ala
500 505

<210> 72

<211> 118

<212> PRT

<213> Homo sapiens

<400> 72

Met Val Gln Lys Ser Arg Asn Gly Val Tyr Pro Gly Pro Ser Gly
1 5 10 15

Glu Lys Lys Leu Lys Val Gly Phe Val Gly Leu Asp Pro Gly Ala Pro
20 25 30

Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro
35 40 45

Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
50 55 60

SequencesSSCPre-file7August03.ST25.txt

Gly Lys Pro Pro Gln Ala Gln Arg Leu Leu Pro Gln Ala Ala Glu Phe
65 70 75 80

Pro Leu Gln Arg Ala Gly Ala Ala Arg Leu Gly Val His Leu Pro
85 90 95

Arg Leu Arg Val Pro Pro Gly Phe Leu Leu Pro Arg Ala Val Cys Val
100 105 110

Phe His His Gln Gly Val
115

<210> 73
<211> 854
<212> PRT
<213> Homo sapiens

<400> 73

Met Val Gln Lys Ser Arg Asn Gly Gly Val Tyr Pro Gly Pro Ser Gly
1 5 10 15

Glu Lys Lys Leu Lys Val Gly Phe Val Gly Leu Asp Pro Gly Ala Pro
20 25 30

Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro
35 40 45

Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
50 55 60

Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
65 70 75 80

Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
85 90 95

Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe
100 105 110

Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile
115 120 125

SequencesSSCPre-file7August03.ST25.txt

Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg
130 135 140

Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg
145 150 155 160

Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu
165 170 175

Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe
180 185 190

Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met
195 200 205

Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val
210 215 220

Val Tyr Ala His Ser Lys Glu Leu Val Thr Ala Trp Tyr Ile Gly Phe
225 230 235 240

Leu Cys Leu Ile Leu Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Gly
245 250 255

Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu
260 265 270

Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gin Thr Trp
275 280 285

Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe
290 295 300

Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val
305 310 315 320

Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala
325 330 335

Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser
340 345 350

SequencesSSCPre-file7August03.ST25.txt

Gly Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr
355 360 365

Val Pro Met Tyr Ser Ser Gln Thr Gln Thr Tyr Gly Ala Ser Arg Leu
370 375 380

Ile Pro Pro Leu Asn Gln Leu Glu Leu Leu Arg Asn Leu Lys Ser Lys
385 390 395 400

Ser Gly Leu Ala Phe Arg Lys Asp Pro Pro Pro Glu Pro Ser Pro Ser
405 410 415

Gln Lys Val Ser Leu Lys Asp Arg Val Phe Ser Ser Pro Arg Gly Val
420 425 430

Ala Ala Lys Gly Lys Gly Ser Pro Gln Ala Gln Thr Val Arg Arg Ser
435 440 445

Pro Ser Ala Asp Gln Ser Leu Glu Asp Ser Pro Ser Lys Val Pro Lys
450 455 460

Ser Trp Ser Phe Gly Asp Arg Ser Arg Ala Arg Gln Ala Phe Arg Ile
465 470 475 480

Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu Glu Ala Ser Leu Pro Gly
485 490 495

Glu Asp Ile Val Asp Asp Lys Ser Cys Pro Cys Glu Phe Val Thr Glu
500 505 510

Asp Leu Thr Pro Gly Leu Lys Val Ser Ile Arg Ala Val Cys Val Met
515 520 525

Arg Phe Leu Val Ser Lys Arg Lys Phe Lys Glu Ser Leu Arg Pro Tyr
530 535 540

Asp Val Met Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met
545 550 555 560

Leu Ser Arg Ile Lys Ser Leu Gln Ser Arg Val Asp Gln Ile Val Gly
565 570 575

SequencesSSCPRe-file7August03.ST25.txt

Arg Gly Pro Ala Ile Thr Asp Lys Asp Arg Thr Lys Gly Pro Ala Glu
580 585 590

Ala Glu Leu Pro Glu Asp Pro Ser Met Met Gly Arg Leu Gly Lys Val
595 600 605

Glu Lys Gln Val Leu Ser Met Glu Lys Lys Leu Asp Phe Leu Val Asn
610 615 620

Ile Tyr Met Gln Arg Met Gly Ile Pro Pro Thr Glu Thr Glu Ala Tyr
625 630 635 640

Phe Gly Ala Lys Glu Pro Glu Pro Ala Pro Pro Tyr His Ser Pro Glu
645 650 655

Asp Ser Arg Glu His Val Asp Arg His Gly Cys Ile Val Lys Ile Val
660 665 670

Arg Ser Ser Ser Ser Thr Gly Gln Lys Asn Phe Ser Ala Pro Pro Ala
675 680 685

Ala Pro Pro Val Gln Cys Pro Pro Ser Thr Ser Trp Gln Pro Gln Ser
690 695 700

His Pro Arg Gln Gly His Gly Thr Ser Pro Val Gly Asp His Gly Ser
705 710 715 720

Leu Val Arg Ile Pro Pro Pro Ala His Glu Arg Ser Leu Ser Ala
725 730 735

Tyr Gly Gly Asn Arg Ala Ser Met Glu Phe Leu Arg Gln Glu Asp
740 745 750

Thr Pro Gly Cys Arg Pro Pro Glu Gly Thr Leu Arg Asp Ser Asp Thr
755 760 765

Ser Ile Ser Ile Pro Ser Val Asp His Glu Glu Leu Glu Arg Ser Phe
770 775 780

Ser Gly Phe Ser Ile Ser Gln Ser Lys Glu Asn Leu Asp Ala Leu Asn

785

SequencesSSCPre-file7August03.ST25.txt
790 795

800

Ser Cys Tyr Ala Ala Val Ala Pro Cys Ala Lys Val Arg Pro Tyr Ile
805 810 815

Ala Glu Gly Glu Ser Asp Thr Asp Ser Asp Leu Cys Thr Pro Cys Gly
820 825 830

Pro Pro Pro Arg Ser Ala Thr Gly Glu Gly Pro Phe Gly Asp Val Gly
835 840 845

Trp Ala Gly Pro Arg Lys
850

<210> 74
<211> 429

<212> PRT

<213> Homo sapiens

<400> 74

Met Val Gln Lys Ser Arg Asn Gly Gly Val Tyr Pro Gly Pro Ser Gly
1 5 10 15

Glu Lys Lys Leu Lys Val Gly Phe Val Gly Leu Asp Pro Gly Ala Pro
20 25 30

Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro
35 40 45

Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
50 55 60

Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
65 70 75 80

Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
85 90 95

Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe
100 105 110

Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile

SequencesSSCPRe-file7August03.ST25.txt
115 120 125

Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg
130 135 140

Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg
145 150 155 160

Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu
165 170 175

Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe
180 185 190

Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met
195 200 205

Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val
210 215 220

Val Tyr Ala His Ser Lys Glu Leu Val Thr Ala Trp Tyr Ile Gly Phe
225 230 235 240

Leu Cys Leu Ile Leu Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Gly
245 250 255

Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu
260 265 270

Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp
275 280 285

Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe
290 295 300

Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val
305 310 315 320

Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala
325 330 335

SequencesSSCPRe-file7August03.ST25.txt

Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser
340 345 350

Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr
355 360 365

Val Pro Met Tyr Ser Ser Gln Thr Gln Thr Tyr Gly Ala Ser Arg Leu
370 375 380

Ile Pro Pro Leu Asn Gln Leu Glu Leu Leu Arg Asn Leu Lys Ser Lys
385 390 395 400

Ser Gly Leu Ala Phe Arg Lys Asp Pro Pro Pro Glu Pro Ser Pro Ser
405 410 415

Gln Lys Val Ser Leu Lys Asp Arg Val Phe Ser Ser Pro
420 425

<210> 75

<211> 854

<212> PRT

<213> Homo sapiens

<400> 75

Met Val Gln Lys Ser Arg Asn Gly Gly Val Tyr Pro Gly Pro Ser Gly
1 5 10 15

Glu Lys Lys Leu Lys Val Gly Phe Val Gly Leu Asp Pro Gly Ala Pro
20 25 30

Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro
35 40 45

Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
50 55 60

Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
65 70 75 80

Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
85 90 95

SequencesSSCPre-file7August03.ST25.txt

Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe
100 105 110

Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile
115 120 125

Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg
130 135 140

Ile Trp Ala Ala Gly Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg
145 150 155 160

Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu
165 170 175

Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe
180 185 190

Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met
195 200 205

Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val
210 215 220

Val Tyr Ala His Ser Lys Glu Leu Val Thr Ala Trp Tyr Ile Gly Phe
225 230 235 240

Leu Cys Leu Ile Leu Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Gly
245 250 255

Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu
260 265 270

Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp
275 280 285

Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe
290 295 300

Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val
305 310 315 320

SequencesSSCPRe-file7August03.ST25.txt

Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala
325 330 335

Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser
340 345 350

Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr
355 360 365

Val Pro Met Tyr Ser Ser Gln Thr Gln Thr Tyr Gly Ala Ser Arg Leu
370 375 380

Ile Pro Pro Leu Asn Gln Leu Glu Leu Leu Arg Asn Leu Lys Ser Lys
385 390 395 400

Ser Gly Leu Ala Phe Arg Lys Asp Pro Pro Pro Glu Pro Ser Pro Ser
405 410 415

Gln Lys Val Ser Leu Lys Asp Arg Val Phe Ser Ser Pro Arg Gly Val
420 425 430

Ala Ala Lys Gly Lys Gly Ser Pro Gln Ala Gln Thr Val Arg Arg Ser
435 440 445

Pro Ser Ala Asp Gln Ser Leu Glu Asp Ser Pro Ser Lys Val Pro Lys
450 455 460

Ser Trp Ser Phe Gly Asp Arg Ser Arg Ala Arg Gln Ala Phe Arg Ile
465 470 475 480

Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu Glu Ala Ser Leu Pro Gly
485 490 495

Glu Asp Ile Val Asp Asp Lys Ser Cys Pro Cys Glu Phe Val Thr Glu
500 505 510

Asp Leu Thr Pro Gly Leu Lys Val Ser Ile Arg Ala Val Cys Val Met
515 520 525

Arg Phe Leu Val Ser Lys Arg Lys Phe Lys Glu Ser Leu Arg Pro Tyr
530 535 540

SequencesSSCPre-file7August03.ST25.txt

Asp Val Met Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met
545 550 555 560

Leu Ser Arg Ile Lys Ser Leu Gin Ser Ser Val Asp Gln Ile Val Gly
565 570 575

Arg Gly Pro Ala Ile Thr Asp Lys Asp Arg Thr Lys Gly Pro Ala Glu
580 585 590

Ala Glu Leu Pro Glu Asp Pro Ser Met Met Gly Arg Leu Gly Lys Val
595 600 605

Glu Lys Gln Val Leu Ser Met Glu Lys Lys Leu Asp Phe Leu Val Asn
610 615 620

Ile Tyr Met Gln Arg Met Gly Ile Pro Pro Thr Glu Thr Glu Ala Tyr
625 630 635 640

Phe Gly Ala Lys Glu Pro Glu Pro Ala Pro Pro Tyr His Ser Pro Glu
645 650 655

Asp Ser Arg Glu His Val Asp Arg His Gly Cys Ile Val Lys Ile Val
660 665 670

Arg Ser Ser Ser Ser Thr Gly Gln Lys Asn Phe Ser Ala Pro Pro Ala
675 680 685

Ala Pro Pro Val Gln Cys Pro Pro Ser Thr Ser Trp Gln Pro Gln Ser
690 695 700

His Pro Arg Gln Gly His Gly Thr Ser Pro Val Gly Asp His Gly Ser
705 710 715 720

Leu Val Arg Ile Pro Pro Pro Ala His Glu Arg Ser Leu Ser Ala
725 730 735

Tyr Gly Gly Asn Arg Ala Ser Met Glu Phe Leu Arg Gln Glu Asp
740 745 750

Thr Pro Gly Cys Arg Pro Pro Glu Gly Thr Leu Arg Asp Ser Asp Thr

SequencesSSCPre-file7August03.ST25.txt
755 760 765

Ser Ile Ser Ile Pro Ser Val Asp His Glu Glu Leu Glu Arg Ser Phe
770 775 780

Ser Gly Phe Ser Ile Ser Gln Ser Lys Glu Asn Leu Asp Ala Leu Asn
785 790 795 800

Ser Cys Tyr Ala Ala Val Ala Pro Cys Ala Lys Val Arg Pro Tyr Ile
805 810 815

Ala Glu Gly Glu Ser Asp Thr Asp Ser Asp Leu Cys Thr Pro Cys Gly
820 825 830

Pro Pro Pro Arg Ser Ala Thr Gly Glu Gly Pro Phe Gly Asp Val Gly
835 840 845

Trp Ala Gly Pro Arg Lys
850

<210> 76
<211> 854
<212> PRT
<213> Homo sapiens
<400> 76

Met Val Gln Lys Ser Arg Asn Gly Gly Val Tyr Pro Gly Pro Ser Gly
1 5 10 15

Glu Lys Lys Leu Lys Val Gly Phe Val Gly Leu Asp Pro Gly Ala Pro
20 25 30

Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro
35 40 45

Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
50 55 60

Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
65 70 75 80

Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
Page 217

SequencesSSCPre-file7August03.ST25.txt

85

90

95

Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe
100 105 110

Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile
115 120 125

Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg
130 135 140

Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg
145 150 155 160

Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu
165 170 175

Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe
180 185 190

Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met
195 200 205

Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val
210 215 220

Val Tyr Ala His Ser Lys Glu Leu Val Thr Ala Trp Tyr Ile Gly Phe
225 230 235 240

Leu Cys Leu Ile Leu Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Gly
245 250 255

Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu
260 265 270

Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp
275 280 285

Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe
290 295 300

SequencesSSCPre-file7August03.ST25.txt

Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val
305 310 315 320

Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala
325 330 335

Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser
340 345 350

Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr
355 360 365

Val Pro Met Tyr Ser Ser Gln Thr Gln Thr Tyr Gly Ala Ser Arg Leu
370 375 380

Ile Pro Pro Leu Asn Gln Leu Glu Leu Leu Arg Asn Leu Lys Ser Lys
385 390 395 400

Ser Gly Leu Ala Phe Arg Lys Asp Pro Pro Pro Glu Pro Ser Pro Ser
405 410 415

Gln Lys Val Ser Leu Lys Asp Arg Val Phe Ser Ser Pro Arg Gly Val
420 425 430

Ala Ala Lys Gly Lys Gly Ser Pro Gln Ala Gln Thr Val Arg Arg Ser
435 440 445

Pro Ser Ala Asp Gln Ser Leu Glu Asp Ser Pro Ser Lys Val Pro Lys
450 455 460

Ser Trp Ser Phe Gly Asp Arg Ser Arg Ala Arg Gln Ala Phe Arg Ile
465 470 475 480

Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu Glu Ala Ser Leu Pro Gly
485 490 495

Glu Asp Ile Val Asp Asp Lys Ser Cys Pro Cys Glu Phe Val Thr Glu
500 505 510

Asp Leu Thr Pro Gly Leu Lys Val Ser Ile Arg Ala Val Cys Val Met
515 520 525

SequencesSSCPre-file7August03.ST25.txt

Arg Phe Leu Val Ser Lys Arg Lys Phe Lys Glu Ser Leu Arg Pro Tyr
530 535 540

Asp Val Met Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met
545 550 555 560

Leu Ser Arg Ile Lys Ser Leu Gln Ser Arg Val Asp Gln Ile Val Gly
565 570 575

Arg Gly Pro Ala Ile Thr Asp Lys Asp Arg Thr Lys Gly Pro Ala Glu
580 585 590

Ala Glu Leu Pro Glu Asp Pro Ser Met Met Gly Arg Leu Gly Lys Val
595 600 605

Glu Lys Gln Val Leu Ser Met Glu Lys Lys Arg Asp Phe Leu Val Asn
610 615 620

Ile Tyr Met Gln Arg Met Gly Ile Pro Pro Thr Glu Thr Glu Ala Tyr
625 630 635 640

Phe Gly Ala Lys Glu Pro Glu Pro Ala Pro Pro Tyr His Ser Pro Glu
645 650 655

Asp Ser Arg Glu His Val Asp Arg His Gly Cys Ile Val Lys Ile Val
660 665 670

Arg Ser Ser Ser Ser Thr Gly Gln Lys Asn Phe Ser Ala Pro Pro Ala
675 680 685

Ala Pro Pro Val Gln Cys Pro Pro Ser Thr Ser Trp Gln Pro Gln Ser
690 695 700

His Pro Arg Gln Gly His Gly Thr Ser Pro Val Gly Asp His Gly Ser
705 710 715 720

Leu Val Arg Ile Pro Pro Pro Ala His Glu Arg Ser Leu Ser Ala
725 730 735

Tyr Gly Gly Asn Arg Ala Ser Met Glu Phe Leu Arg Gln Glu Asp
740 745 750

SequencesSSCPRe-file7August03.ST25.txt

Thr Pro Gly Cys Arg Pro Pro Glu Gly Thr Leu Arg Asp Ser Asp Thr
755 760 765

Ser Ile Ser Ile Pro Ser Val Asp His Glu Glu Leu Glu Arg Ser Phe
770 775 780

Ser Gly Phe Ser Ile Ser Gln Ser Lys Glu Asn Leu Asp Ala Leu Asn
785 790 795 800

Ser Cys Tyr Ala Ala Val Ala Pro Cys Ala Lys Val Arg Pro Tyr Ile
805 810 815

Ala Glu Gly Glu Ser Asp Thr Asp Ser Asp Leu Cys Thr Pro Cys Gly
820 825 830

Pro Pro Pro Arg Ser Ala Thr Gly Glu Gly Pro Phe Gly Asp Val Gly
835 840 845

Trp Ala Gly Pro Arg Lys
850